



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 103553

TO: Sharon Turner
Location: CM1/10B09&10B19
Art Unit : 1647
Friday, September 12, 2003

Case Serial Number: 09/978191

From: P. Sheppard
Location: Biotech-Chem Library
CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

103 553

From: Turner, Sharon
Sent: Wednesday, September 10, 2003 1:19 PM
To: STIC-Biotech/ChemLib
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Please search CDB and interference files

AA SEQ ID NO:506

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CM1-10B09
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Biotechnology GAU 1647
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Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 9/12/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
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Sequence Sys.: _____
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Other (specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:10:02; Search time 95 Seconds

(without alignments)
741.562 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505

Sequence: 1 MRGSEVLLMWLLVAVGST.....SEQISFLSEQGSCSKXDS 273

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1505	100.0	273	4 Q96EG0	Q96EG0 homo sapien
2	1504	99.9	273	4 Q9UHF1	Q9UHF1 homo sapien
3	1180	78.4	278	11 Q9QXN5	Q9QXN5 mus musculu
4	1103.5	73.3	265	11 Q9DCPS	Q9DCPS mus musculu
5	727.5	48.3	190	11 Q9JXW3	Q9JXW3 mus musculu
6	435.5	28.9	293	11 Q35447	Q35447 mus musculu
7	423.5	28.1	293	4 Q99944	Q99944 mus musculu
8	420.5	27.9	293	4 Q8IV30	Q8IV30 homo sapien
9	277.5	18.4	509	5 Q9VZD0	Q9VZD0 dirosophila
10	277.5	18.4	512	5 Q9SRQ1	Q9SRQ1 dirosophila
11	256	17.0	1574	11 Q88281	Q88281 rattus norv
12	252.5	16.8	558	4 Q9UJF6	Q9UJF6 homo sapien
13	251.5	16.7	553	4 Q9VJL7	Q9VJL7 homo sapien
14	251.5	16.7	553	4 Q8IUX8	Q8IUX8 homo sapien
15	251.5	16.7	554	4 Q9NY67	Q9NY67 homo sapien
16	249.5	16.6	553	4 Q8NBV0	Q8NBV0 homo sapien

17	245.5	16.3	327	11 Q8BPM8	Q8BPM8 mus musculu
18	245.5	16.3	550	11 Q9JZT5	Q9JZT5 mus musculu
19	225.5	15.0	544	13 Q8AVH7	Q8AVH7 xenopus lae
20	223	14.8	561	11 Q91V88	Q91V88 mus musculu
21	218.5	14.5	578	11 Q81ZD3	Q81ZD3 mus musculu
22	218	14.5	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi
23	217.5	14.5	528	11 Q9CXD8	Q9CXD8 mus musculu
24	198	13.2	747	11 Q8VHP4	Q8VHP4 mus musculu
25	198	13.2	1004	11 Q8CGA7	Q8CGA7 mus musculu
26	198	13.2	1034	11 Q8VH17	Q8VH17 mus musculu
27	197.5	13.1	592	11 Q91X15	Q91X15 mus musculu
28	196	13.0	1034	11 Q8V1K5	Q8V1K5 mus musculu
29	194.5	12.9	590	11 Q8C088	Q8C088 mus musculu
30	193	12.8	609	4 Q923JF5	Q923JF5 mus musculu
31	189	12.6	678	4 Q14393	Q14393 homo sapien
32	185.5	12.3	1600	11 Q8K4G0	Q8K4G0 mus musculu
33	185.5	12.3	1666	11 Q8K4G1	Q8K4G1 mus musculu
34	184.5	12.3	2906	11 Q9W0H9	Q9W0H9 rattus norv
35	184	12.2	673	11 Q61592	Q61592 mus musculu
36	184	12.2	674	11 Q99K57	Q99K57 mus musculu
37	183.5	12.2	784	11 Q8BM43	Q8BM43 mus musculu
38	183.5	12.2	816	11 Q8R417	Q8R417 rattus norv
39	183.5	12.2	858	11 Q8BM06	Q8BM06 mus musculu
40	182.5	12.1	815	4 Q96J52	Q96J52 homo sapien
41	181.5	12.1	648	5 Q9VJY4	Q9VJY4 dirosophila
42	181.5	12.1	648	5 Q9NKD7	Q9NKD7 dirosophila
43	181	12.0	299	11 Q8BX64	Q8BX64 mus musculu
44	181	12.0	1764	11 Q35806	Q35806 rattus norv
45	181	12.0	2809	4 Q96J98	Q96J98 homo sapien

ALIGNMENTS

RESULT 1

ID	Q96EG0	PRELIMINARY;	PRT;	273 AA.
AC	Q96EG0;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Similar to NEU1 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RA	Strasbourg R.;			
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC012377; AAH12377.1; -			
DR	InterPro; IPR00152; Aex_Hydroxyl.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF_Like.			
DR	Pfam; PF00008; EGF_2.			
DR	SMART; SM00179; EGF_CA_1.			
DR	PROSITE; PS00010; AEX_HYDROXYL; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; 1.			
DR	PROSITE; PS01187; EGF_CA; 1.			
KW	EGF-like domain.			
SO	SEQUENCE 273 AA; 29631 MW; SMD0A4845ED5B688 CRC64;			
Query Match	100.0%;	Score 1505;	DB 4;	Length 273;
Best Local Similarity	100.0%;	Pred. No. 1.5e-127;		
Matches 273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1 MRGSEVLLMWLLVAVGTEHAHRRRCRCVCAVRAHGDPSSESVQCVQVQPFLLTCGHR 60
Db	1 MRGSEVLLMWLLVAVGTEHAHRRRCRCVCAVRAHGDPSSESVQCVQVQPFLLTCGHR 60
Qy	61 ACSTYRTYTAARSPGLAPARPRVACPGWKRTSLPGACGAICOPPCRNQSGSCVOP 120

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Db . 61 ACSTYRTITRYAYRRSPGLAPAPRRVACCPGKRTISGLPGACGAALCPPCRNGSCVOP 120
OY 121 GRGCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 180
Db 121 GRGCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 180
OY 181 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 240
Db 181 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 240
OY 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273

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RESULT 2

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O9UHFI PRELIMINARY; PRT; 273 AA.
AC O9UHFI;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN NOTCH4-like protein (Hypothetical protein).
OS ZNEU1 OR DKFZP586L2317.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.,
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF186111; AAF01429.1; -
DR HSSP; P08709; IPAK.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00179; EGF_CA_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF_1; 1.
DR PROSITE; PS01187; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA_1.
KW Hydrothetical protein; EGF-like domain.
SQ SEQUENCE 273 AA; 29617 MW; 5740BB845BD5A988 CRC64;

```

Query Match 99.9%; Score 1504; DB 4; Length 273;
 Best Local Similarity 99.6%; Pred. No. 1.8e-127;
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNGSQEVLIMLMLVLAAGGTEHAAYRGRVCAVRHAGDPVSSFFQRYVQPPFLTTCDGHR 60
Db 1 MNGSQEVLIMLMLVLAAGGTEHAAYRGRVCAVRHAGDPVSSFFQRYVQPPFLTTCDGHR 60
OY 61 ACSTYRTITRYAYRRSPGLAPAPRRVACCPGKRTISGLPGACGAALCPPCRNGSCVOP 120
Db 61 ACSTYRTITRYAYRRSPGLAPAPRRVACCPGKRTISGLPGACGAALCPPCRNGSCVOP 120
OY 121 GRGCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 180
Db 121 GRGCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 180
OY 181 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 240
Db 181 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 240

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OY 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273

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RESULT 3

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O9QXT5 PRELIMINARY; PRT; 278 AA.
AC O9QXT5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN NOTCH4-like protein (Vascular endothelial zinc finger 1).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RL "Mus musculus homolog of HLA class III region containing NOTCH4
RT gene.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Liver;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184973; AAF01322.1; -
DR EMBL; BC024610; AAH24610.1; -
DR HSSP; P00740; IEDM.
DR MGP; MGI:1313291; Vezfl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA_1.
KW EGF-like domain.
SQ SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

```

Query Match 78.4%; Score 1180; DB 11; Length 278;
 Best Local Similarity 77.7%; Pred. No. 2.9e-98;
 Matches 213; Conservative 19; Mismatches 40; Indels 2; Gaps 2;

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OY 1 MNGSQEVLIMLMLVLAAGGTEHAAYRGRVCAVRHAGDPVSSFFQRYVQPPFLTTCDGHR 59
Db 4 MNGSQEVLIMLMLVLAAGGTEHAAYRGRVCAVRHAGDPVSSFFQRYVQPPFLTTCDGHR 59
OY 61 ACSTYRTITRYAYRRSPGLAPAPRRVACCPGKRTISGLPGACGAALCPPCRNGSCVOP 119
Db 61 ACSTYRTITRYAYRRSPGLAPAPRRVACCPGKRTISGLPGACGAALCPPCRNGSCVOP 119
OY 120 PGRCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 179
Db 124 PGRCPAGMGDTQOSVDVDECSARRGCCPQRCINTAGSYWCQCEGHSISADGTLCPVK 179
OY 180 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 238
Db 184 GPPRVANPTGVDSAMKEEVORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSL 238
OY 239 LVHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 272
Db 239 LVHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 272

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Db 244 ILAHSFQOLDRIDSLSEQVSLFLEHLGSCSCKKD 277

RESULT 4

ID Q9DCP5 PRELIMINARY; PRT; 265 AA.

AC Q9DCP5; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vascular endothelial zinc finger 1.
GN Vezfl.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gueirinch S., Hill D., Hofmann M., Hume D.A., Kamija M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK002601; BAB22222.1; -.
DR HSSP; P00740; 1EDM.
DR MGB; MGI:1313291; Vezfl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA884FF97E CRC64;

Query Match

Best Local Similarity 73.3%; Score 1103.5; DB 11; Length 265;
Matches 202; Conservative 18; Mismatches 39; Indels 15; Gaps 3;

QY 1 MEGSEVLLMLVLAVGG-TEHAYRPGRRVCAVNAHGDVSESFVQRYQPFLLTTCQGH 59
Db 4 MWGSGELLVAMFLVLAADGTEHAYRPSRRVCTVSGISGSISETFQRYQPYLLTTCQGH 63
QY 60 RACSTYRTTYRATVRRSGRLAPRRVACCPGWRKTSGLPGACGALICQPPRNGSCVQ 119
Db 64 RACSTYRTTYRATVRRSGRLAPRRVACCPGWRKTSGLPGACGALICQPPRNGSCVQ 123
QY 120 PGRCPAGWGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVK 179
Db 124 PGRCPAGWGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVK 183
QY 180 GGPVAVNPNT-GVDSAMKEEVQRLQSRVLLLEKQLQVLAPLHSLASQALEHGLPDCS 238
Db 184 GGPVAVNPNT-GVDSAMKEEVQRLQSRVLLLEKQLQVLAPLHSLASQALEHGLPDCS 243

QY 239 ILAHSFQOLDRIDSLSEQVSLFLEHLGSCSCKKD 272
Db 244 ILAHSFQOLDRIDSLSEQVSLFLEHLGSCSCKKD 264

RESULT 5

ID Q9JRW3 PRELIMINARY; PRT; 190 AA.

AC Q9JRW3; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CBL20.
GN CBL20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;

SEQUENCE FROM N.A.

RP TISSUE=Spleen.
RC Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.;
RT "Cloning and Characterization of a Novel 20.4kD Estrogen-regulated
RL protein in the Rat Spleen."
RN Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen.
RA Marcantonio D., Huynh H.T.;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF223678; AAF3352.1; -.
DR InterPro; IPR00152; Asx hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1E998 CRC64;

Query Match

Best Local Similarity 48.3%; Score 727.5; DB 11; Length 190;
Matches 130; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 105 AICPPCNRNGSCVQPGRCPCAGWGDTCQSDVDECSARRGGCPQRCINTAGSYWCQW 164
Db 21 AICPPCNRNGSCVQPGRCPCAGWGDTCQSDVDECSARRGGCPQRCINTAGSYWCQW 80
QY 165 EGHSLADGTLCPVKGPPVAVNPNT-GVDSAMKEEVQRLQSRVLLLEKQLQVLAPLH 223
Db 81 EGHSLADGTLCPVKGPPVAVNPNT-GVDSAMKEEVQRLQSRVLLLEKQLQVLAPLH 140
QY 224 LASQALEHGLPDCSGLVHVSFQOLGRITSLSEQVSLFLEHLGSCSCKKD 272
Db 141 LASQALEHGLPDCSGLVHVSFQOLGRITSLSEQVSLFLEHLGSCSCKKD 189
RESULT 6
ID Q35447 PRELIMINARY; PRT; 293 AA.
AC Q35447; 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 32.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

RP . SEQUENCE FROM N.A.
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,
 RT "Sequence of the mouse major histocompatibility locus class III
 region."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030001; AAB82010.1; -
 DR HSP: P35555; IEMN.
 DR InterPro: IPR00152; Asx hydroxyl.
 DR InterPro: IPR01881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR Pfam: PF00008; EGF; 2; -
 DR SMART: SM00179; EGF_CA; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 KW Hypothetical protein; EGF_Like domain.
 SQ SEQUENCE 293 AA; 32066 MW; 8A99A5EC000A2C62 CRC64;

Query Match 28.9%; Score 435.5; DB 11; Length 293;
 Best Local Similarity 37.3%; Pred. No. 3.5e-31;
 Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;
 QY 1 MRGQEVLLMWLVLAAG-GTE-HAYRPRRCVAVRAHGDV--SESPVQRYVQFLLTTC 56
 DB 11 LRG-----LSFPLVMTGECTRGSGFRKESIGVCSKQTLVPLRVESYSQPYKRYLTLC 65
 QY 57 DGHACSTYRTYRTAVRSPGLAPRPVYACCPGKRTSGLPAGCA-AICQPPCNGG 115
 DB 66 AGRRICSTYRTYRTAVRSPGLAPRPVYACCPGKRTSGLPAGCA-AICQPPCNGG 115
 QY 116 SCVQPRRCPCAPMRSDTQSDVDECSARGGCPRCINTAGSYWCQWEGHSLSDGTL 175
 DB 123 VCTGPRRCPCAPMRSDTQSDVDECSARGGCPRCINTAGSYWCQWEGHSLSDGTL 175
 QY 176 CVKGGPRVAVNPVGV-----DSAMKEVQRLQSRVLLLEKQLVLAAPL 221
 DB 183 CA--GGPR--SPTSASITLVAAREADSEERALLRWEVALLRLEKLLQ----- 228
 QY 222 HSLASQA--LEHGLP-DPGSLVHSFOQL-----GRDLSLSEQISFLLEQSGSCCKKDS 273
 DB 229 --WATQAGWVRAVLPMPPELRPEQVAVELMGDRDRLIESDVLLEERLIGACSCEDNS 286

RESULT 7
 ID 099944 PRELIMINARY; PRT; 293 AA.
 AC 099944.
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
 RA Banta A., Spies T., Hood L.,
 RT "Sequence determination of 300 kilobases of the human class III MHC
 locus."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U89336; AAB47494.1; -
 DR HSP: P35555; IEMN.
 DR GeneW: HGNC:13944; Ceorf8.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR Pfam: PF00008; EGF; 2; -
 DR SMART: SM00179; EGF_CA; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 KW EGF_Like domain.
 SQ SEQUENCE 293 AA; 32262 MW; 6519CA254FB23FD0 CRC64;

Query Match 28.1%; Score 423.5; DB 4; Length 293;
 Best Local Similarity 36.5%; Pred. No. 4.2e-30;
 Matches 103; Conservative 37; Mismatches 107; Indels 35; Gaps 10;
 QY 12 LVLVAVGTEHAYRPRRCVAVRAHGDV--SESPVQRYVQFLLTTCGHACSTYRTY 69
 DB 19 LILPBGAKGSLREESQVCSKQTLVPLRVESYSQPYKRYLTLCAGRRICSTYRTY 78
 QY 70 RTAVRSPGLAPRPVYACCPGKRTSGLPAGCA--CGAATCQPPCNGGSCVQPRCPCP 127
 DB 79 RVWM-REVRREVQVTHAVCCQWKKRH--PGALTC-EAICAKPCLNGVAVRDPQCECAP 134
 QY 128 GMRGDTQSDVDECSARAGGCPRCINTAGSYWCQWEGHSLSDGTLVCPKGGPRVAV 187
 DB 135 GMGKXCHVDVDECRSTITLCSHCFNTAGSFTGCPHDVLGVDGRTCWEGSPPEPTSA 194
 QY 188 NPTGV-----DSAMKEVQRLQSRVLLLEKQLVLAAPLHSLASQA--LEHGLP-D 235
 DB 195 SILSVAVRAEKDRLAKQEIHELGRLERLQ-----WAGQAGWVRAVLPVP 243
 QY 236 PGLSLVHSFOQL-----GRDLSLSEQISFLLEQSGSCCKKDS 273
 DB 244 PEELOPEVAVLMWGRGRLIESDVLLEERLIGACSCEDNS 285

RESULT 8
 ID 081V30 PRELIMINARY; PRT; 293 AA.
 AC 081V30.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 OS Chromosome 6 open reading frame 8.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Tissue=Brain;
 RA Straussberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC035574; AAB35574.1; -
 SQ SEQUENCE 293 AA; 32261 MW; 6519CA25568FFD0 CRC64;

Query Match 27.9%; Score 420.5; DB 4; Length 293;
 Best Local Similarity 36.2%; Pred. No. 7.7e-30;
 Matches 102; Conservative 38; Mismatches 107; Indels 35; Gaps 10;
 QY 12 LVLVAVGTEHAYRPRRCVAVRAHGDV--SESPVQRYVQFLLTTCGHACSTYRTY 69
 DB 19 LILPBGAKGSLREESQVCSKQTLVPLRVESYSQPYKRYLTLCAGRRICSTYRTY 78
 QY 70 RTAVRSPGLAPRPVYACCPGKRTSGLPAGCA--CGAATCQPPCNGGSCVQPRCPCP 127
 DB 79 RVWM-REVRREVQVTHAVCCQWKKRH--PGALTC-EAICAKPCLNGVAVRDPQCECAP 134
 QY 128 GMRGDTQSDVDECSARAGGCPRCINTAGSYWCQWEGHSLSDGTLVCPKGGPRVAV 187
 DB 135 GMGKXCHVDVDECRSTITLCSHCFNTAGSFTGCPHDVLGVDGRTCWEGSPPEPTSA 194
 QY 188 NPTGV-----DSAMKEVQRLQSRVLLLEKQLVLAAPLHSLASQA--LEHGLP-D 235
 DB 195 SILSVAVRAEKDRLAKQEIHELGRLERLQ-----WAGQAGWVRAVLPVP 243
 QY 236 PGLSLVHSFOQL-----GRDLSLSEQISFLLEQSGSCCKKDS 273

Db 244 PEELOPEVALMGDRISLSDVLLQERLACSCEDNS 285

RESULT 9

09VZD0 PRELIMINARY; PRT; 509 AA.

AC 09VZD0; 241-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE CG7447 protein.

GN CG7447.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OC NCB1_TaxId=7227;

OX NCB1_TaxId=7227;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G., Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Balwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.V., Bouck J., Brokstein P., Broctier P., Butris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dwyer A.D., Dew I., Dietz S.M., Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferrelira S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Hayery D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei J.B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shu B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "the genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

DR EMBL; AE003481; AAF47894.1; -

DR HSSP; P00740; 1EDM.

DR FLYBase; FBgn0035539; CG7447.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF00008; EGF_2.

DR SMART; SM00179; EGF_CA_1.

DR PROSITE; PS00010; ASX_HYDROXYL_1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA_1.

KW EGF-like domain.

SO SEQUENCE 509 AA; 57413 MW; FE4782EA6E121F0 CRC64;

Query Match 18.4%; Score 277.5; DB 5; Length 509;

Best Local Similarity 27.8%; Pred. No. 1,1e-16;

Matches 73; Conservative 40; Mismatches 113; Indels 37; Gaps 9;

QY 28 RRVCAVRAHGDPPV--SESPVQRYVQPELTTCD----GHRACSTYRTYRTAYRRSPGLA 80

DB RHICQQRRTVMPVVRTEVRSRPTWKIVATPCQPTFGSQCTRRQVAVHEDAVRVIDHK 301

QY 81 PARP-RYACCGKRTSLGPAACGALIQPFCRNAGSCVQGRCRCPMGMTGTCQSYVD 139

DB TAQQMTYDCCGWSNENRSDSCMKPICSARCONGNCTAPSTCSCPFTGRFCEQDVPD 361

QY 140 ECSARGGCPQRCINTAGSYWCQCEGHSLSADGTLCPKGGPPVAVN-----P 189

DB ECQTEK-PCDQCCINTHOSYFCRCRGVLSDDQSC-----KVVSTNADDAFARDLE 414

QY 190 TGVDSAMEEVQRLQS-----RVLDLEKQLQVLAPLHSLASQ--ALEHGLPDPG 237

DB NDIDDTDAEVATRLQKIEKSLANERVHTNELQKSLQATYSVVDTLKSLSTLEKQADQV 474

QY 238 SLVHSFQQLGRIDSLSEQISFL 260

DB RLQTNLYKTESRTYKLEGMNML 497

RESULT 10

ID 095R01 PRELIMINARY; PRT; 512 AA.

AC 095R01;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE LD16414P.

GN CG7447.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OC NCB1_TaxId=7227;

OX NCB1_TaxId=7227;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuno J., Pauley J., Paragas V., Park S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celinker S.

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY061220; AA128768.1; -

DR FLYBase; FBgn0035539; CG7447.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF00008; EGF_2.

DR SMART; SM00179; EGF_CA_1.

DR PROSITE; PS00010; ASX_HYDROXYL_1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA_1.

KW EGF-like domain.

SO SEQUENCE 512 AA; 57770 MW; 4DD372E4A6FE7627 CRC64;

Query Match 18.4%; Score 277.5; DB 5; Length 512;

Best Local Similarity 27.8%; Pred. No. 1,1e-16;

Matches 73; Conservative 40; Mismatches 113; Indels 37; Gaps 9;

QY 28 RRVCAVRAHGDPPV--SESPVQRYVQPELTTCD----GHRACSTYRTYRTAYRRSPGLA 80

DB RHICQQRRTVMPVVRTEVRSRPTWKIVATPCQPTFGSQCTRRQVAVHEDAVRVIDHK 304

QY 81 PARP-RYACCGKRTSLGPAACGALIQPFCRNAGSCVQGRCRCPMGMTGTCQSYVD 139

DB TAQQMTYDCCGWSNENRSDSCMKPICSARCONGNCTAPSTCSCPFTGRFCEQDVPD 361

QY 140 ECSARGGCPQRCINTAGSYWCQCEGHSLSADGTLCPKGGPPVAVN-----P 189

DB ECQTEK-PCDQCCINTHOSYFCRCRGVLSDDQSC-----KVVSTNADDAFARDLE 414

QY 190 TGVDSAMEEVQRLQS-----RVLDLEKQLQVLAPLHSLASQ--ALEHGLPDPG 237

DB NDIDDTDAEVATRLQKIEKSLANERVHTNELQKSLQATYSVVDTLKSLSTLEKQADQV 474

QY 238 SLVHSFQQLGRIDSLSEQISFL 260

DB RLQTNLYKTESRTYKLEGMNML 497

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Db      305 TAAQMTYDCCTGMSSENPRSDSCMKPICARQNGANTASTGSCPTGFGRCEDVD
QY      140 EBSARRGGCPORCITAGSYWCQMEGHSLSADGTLVCPKGGPRVAPN-----P 189
Db      365 ECOTER-PCDDOCINTHTSYFCRCRQGFVLOSDDQSC-----KVVSTNADAEARDLE 417
QY      190 TGVDSAMKEVYORLOS-----RVDLLEKLOVLAPLHSLAQ--ALEHGLDDPG 237
Db      418 NDIDDTDAEVAFLRLOKIERKSLANEVYHNELOKSLQATYVVDTLKSLSTLEKQADVS 477
QY      238 SLVHVSFOQLGRIDSLSEQISFL 260
Db      478 RLQTNLYKTESRTNLEGMNLL 500

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RESULT 11

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ID      088281      PRELIMINARY;      PRT;      1574 AA.
AC      088281;
DT      01-NOV-1998 (TREMBlrel. 08, Created)
DT      01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      MEGF6.
GN      MEGF6.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]
RP      NCB1_TaxID=10116;
RC      SEQUENCE FROM N.A.
RX      STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=98360089; PubMed=9693030;
RA      Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT      "Identification of high-molecular-weight proteins with multiple EGF-
RL      like motifs by motif-trap screening.";
DR      EMBL: AB011532; BAA32462.1; -
HSSP; P00736; IAPQ.
DR      InterPro: IPR00152; Asx_hydroxyl.
DR      InterPro: IPR001881; EGF_Ca.
DR      InterPro: IPR006209; EGF_like.
DR      InterPro: IPR002049; Laminin_EGF.
DR      Pfam: PF00008; EGF_24.
DR      PRINTS: PR00011; EGF_LAMININ.
DR      SMART: SM00179; EGF_CA_4.
DR      PROSITE: PS00010; ASX_HYDROXYL; 5.
DR      PROSITE: PS00022; EGF_1; 23.
DR      PROSITE: PS01186; EGF_2; 23.
DR      PROSITE: PS01187; EGF_CA; 5.
KW      EGF-like domain.
SQ      SEQUENCE 1574 AA; 165445 MW; 2B48533DBF77FE67 CRC64;

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Query Match      17.0%; Score 256; DB 11; Length 1574;
Best Local Similarity 37.9%; Pred. No. 3.3e-14;
Matches 64; Conservative 16; Mismatches 61; Indels 28; Gaps 9;

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QY      30 VCAVR-----AHGDPVSESFVQRYVPELITTCGHRAC--STYRTITAYRRSGFLAPA 82
Db      43 VCAEQCLTVGHROPVQAFSRIVPWRTGCAQOAMCGORRTVYMSYQVVA--TEA 101
QY      83 RPRYACCPGMRKRTSGLPGA-----CGAII--COPPCRN--GGSCVQGRCPGAPGWR-- 130
Db      102 RTVFRCCPGMSQKPGEGCLSLVDEASANGCEGPCCTTVGCF-----YKCPGYOLO 156
QY      131 --GPTQGVDECSARRGGCPORCINTAGSYWCQMEGHSLSADGTLCV 177
Db      157 GPKTKQ--DVDECRANNGCQHRCVNTPGSYLCECKPGRLHTDRTCL 204

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RESULT 12
Q9UFK6      PRELIMINARY;      PRT;      558 AA.
ID      Q9UFK6

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AC      Q9UFK6;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Hypothetical protein (Fragment).
GN      DKFZ564P2063.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      NCB1_TaxID=9606;
RC      SEQUENCE FROM N.A.
RX      TISSUE=Brain;
RA      Duesterhoeft A., Lauber J., Mewes H.W., Gaassenhuber J., Wiemann S.;
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC      -1 SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR      EMBL: AL117610; CAB56014.1; -
DR      HSSP; P00736; IAPQ.
DR      Genew; HGNC:3235; EGRF6.
DR      InterPro: IPR00152; Asx_hydroxyl.
DR      InterPro: IPR001881; EGF_Ca.
DR      InterPro: IPR006209; EGF_like.
DR      InterPro: IPR000998; MAM_domain.
DR      Pfam: PF00008; EGF_4.
DR      Pfam: PF00629; MAM_1.
DR      SMART; SM00179; EGF_CA_3.
DR      PROSITE: PS00010; ASX_HYDROXYL; 3.
DR      PROSITE: PS00022; EGF_1; 1.
DR      PROSITE: PS01186; EGF_2; 2.
DR      PROSITE: PS01187; EGF_CA; 2.
DR      PROSITE: PS00600; MAM_2; 1.
KW      Hypothetical protein; EGF-like domain; Glycoprotein.
SQ      SEQUENCE 558 AA; 61828 MW; AA38D7DCE402BFA3 CRC64;

```

```

Query Match      16.8%; Score 252.5; DB 4; Length 558;
Best Local Similarity 36.8%; Pred. No. 2.1e-14;
Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7;

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```

QY      58 GHRACSTYRTITRAYRRSGFLAPRPRVACCPGMRKRTSGLPACGAATGCPGRRNGSGC 117
Db      26 GNAASARHHGILASA--RQPVCHYGTKLACCYGMRHNS--KQVC-EATCEPCK-FGRC 79
QY      118 VQPRCRCPAGMRGDTQSPVDDECSARRGGCPORCINTAGSYWCQMEGHSLSADGTLCV 177
Db      80 VGPWKCKCLPGYGTKTSQDVNCGMKPRPCQHRCVNTHSGYKFCLSGHMLMPAT-CV 138
QY      178 -----PKGGP-----RVAPN 188
Db      139 YSRTCAMINQVSCEDTEEGPQCLCPSSGRLAPN 173

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RESULT 13

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ID      Q9NZL7      PRELIMINARY;      PRT;      553 AA.
AC      Q9NZL7;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Epidermal growth factor repeat containing protein.
GN      EGRF6.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      NCB1_TaxID=9606;
RC      SEQUENCE FROM N.A.
RX      MEDLINE=20079166; PubMed=10610727;
RA      Yeung G., Mulero J.J., Berntsen R.P., Loeb D.B., Drmanac R.,
RT      "Cloning of a novel epidermal growth factor repeat containing gene
RL      EGRF6: expressed in tumor and fetal tissues.";
Genomics 62:304-307(1999).

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CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 DR EMBL; AF186084; AAF27812.1; -.
 DR HSSP; P00736; IAPQ.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00629; MAM; 1.
 DR SMART; SM00179; EGF CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF CA; 3.
 DR PROSITE; PS00060; MAM 2; 1.
 KW EGF-like domain; Glycoprotein.
 SQ SEQUENCE 553 AA; 61314 MW; 2FF55F167857DE50 CRC64;

Query Match 16.7%; Score 251.5; DB 4; Length 553;
 Best Local Similarity 36.8%; Pred. No. 2.6e-14;
 Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7;

OY 58 GHRACSTYRTTYRTYRSPGLAPARPRYACCPGKRTSGLPAGCAAIICOPPCRNNGSSC 117
 DB 21 GNAASARHHGLASA--RQPGVCHYGTKLACCYGMRNS--KGYC-EATCEBGCK-FGEC 74
 OY 118 VQPGRCRCPCAGRGDTCQSDVDDECSARRGCGPCRCINTAGSYWCQCGEHSLSADGTLCV 177
 DB 75 VGPNCRCPCPGYTGKTCQSDVDNECGMKRPPCOHRCVNTGSKYKFCLSGHMLMPDAT-CV 133
 OY 178 -----PKGGPP-----RVAAPN 188
 DB 134 NSRTCAMINCOYSCEDTEEGPQCLCPSSGRLAPN 168

RESULT 14
 O8IUX8 PRELIMINARY; PRT; 553 AA.
 AC O8IUX8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to EGF-like-domain, multiple 6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038587; AAH38587.1; -.
 SQ SEQUENCE 553 AA; 61317 MW; 3AE93A0362E861E0 CRC64;

Query Match 16.7%; Score 251.5; DB 4; Length 553;
 Best Local Similarity 36.8%; Pred. No. 2.6e-14;
 Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7;

OY 58 GHRACSTYRTTYRTYRSPGLAPARPRYACCPGKRTSGLPAGCAAIICOPPCRNNGSSC 117
 DB 21 GNAASARHHGLASA--RQPGVCHYGTKLACCYGMRNS--KGYC-EATCEBGCK-FGEC 74
 OY 118 VQPGRCRCPCAGRGDTCQSDVDDECSARRGCGPCRCINTAGSYWCQCGEHSLSADGTLCV 177
 DB 75 VGPNCRCPCPGYTGKTCQSDVDNECGMKRPPCOHRCVNTGSKYKFCLSGHMLMPDAT-CV 133
 OY 178 -----PKGGPP-----RVAAPN 188
 DB 134 NSRTCAMINCOYSCEDTEEGPQCLCPSSGRLAPN 168

RESULT 15

O9NY67
 ID O9NY67; PRELIMINARY; PRT; 554 AA.
 AC O9NY67;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN w80.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Teratocarcinoma, and, Neuron;
 RA Franco B.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Teratocarcinoma, and, Neuron;
 RX MEDLINE=20241927; PubMed=10777661;
 RA Buchner G., Orfaneli U., Quadert N., Baesi M.T., Andolfi G.;
 RT "Identification of a new EGF-repeat-containing gene from human Xp22;
 RT Acandidate for developmental disorders";
 RL Genomics 65:16-23(2000).
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 DR EMBL; AJ245671; CAB92132.1; -.
 DR HSSP; P00736; IAPQ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00629; MAM; 1.
 DR SMART; SM00179; EGF CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF CA; 3.
 DR PROSITE; PS00060; MAM 2; 1.
 KW Hypothetical protein; EGF-like domain; Glycoprotein.
 SQ SEQUENCE 554 AA; 61388 MW; D519238F2A604101 CRC64;

Query Match 16.7%; Score 251.5; DB 4; Length 554;
 Best Local Similarity 36.8%; Pred. No. 2.6e-14;
 Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7;

OY 58 GHRACSTYRTTYRTYRSPGLAPARPRYACCPGKRTSGLPAGCAAIICOPPCRNNGSSC 117
 DB 21 GNAASARHHGLASA--RQPGVCHYGTKLACCYGMRNS--KGYC-EATCEBGCK-FGEC 74
 OY 118 VQPGRCRCPCAGRGDTCQSDVDDECSARRGCGPCRCINTAGSYWCQCGEHSLSADGTLCV 177
 DB 75 VGPNCRCPCPGYTGKTCQSDVDNECGMKRPPCOHRCVNTGSKYKFCLSGHMLMPDAT-CV 133
 OY 178 -----PKGGPP-----RVAAPN 188
 DB 134 NSRTCAMINCOYSCEDTEEGPQCLCPSSGRLAPN 168

Search completed: September 10, 2003, 17:15:14
 Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:09:17; Search time 23 Seconds

(without alignments)
558.187 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505

Sequence: 1 MRGSGEVLMLVLAAGT.....SEQISFLEQLGSCSKKDS 273

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result. No.	Score	Query Match	Query length	ID	Description
1	196	13.0	1964	NTC4_MOUSE	P31695 mus musculus
2	188.5	12.5	2003	NTC4_HUMAN	Q99466 homo sapien
3	185	12.3	816	NEI2_MOUSE	Q61220 mus musculus
4	183.5	12.2	2907	FBN2_MOUSE	Q61555 mus musculus
5	182.5	12.1	816	NEI2_HUMAN	Q99435 homo sapien
6	182	12.1	810	NEI1_HUMAN	Q92832 homo sapien
7	180.5	12.0	816	NEI2_RAT	Q62918 rattus norv
8	180	12.0	810	NEI1_RAT	Q62919 rattus norv
9	176.5	11.7	816	NEI1_CHICK	Q90827 gallus gall
10	176.5	11.7	2871	FBN1_HUMAN	P35555 homo sapien
11	175.5	11.6	2321	NTC3_HUMAN	Q9um47 homo sapien
12	175	11.6	652	CD93_HUMAN	Q9npy3 homo sapien
13	175	11.6	2703	NOTC_HUMAN	P07207 dirosophila
14	173.5	11.5	1247	NIDO_HUMAN	P14543 homo sapien
15	172.5	11.5	2871	FBN1_MOUSE	Q61554 mus musculus
16	172.5	11.4	2531	NTC1_MOUSE	Q01705 mus musculus
17	171.5	11.4	2871	FBN1_BOVIN	P98133 bos taurus
18	170.5	11.3	871	FBN1_PIG	Q9cv36 sus scrofa
19	170	11.3	675	PRTS_MOUSE	Q08761 mus musculus
20	170	11.3	2911	FBN2_HUMAN	P35555 homo sapien
21	169.5	11.3	2318	NTC3_MOUSE	Q61982 mus musculus
22	169	11.2	833	DL_DROME	P10041 dirosophila
23	168	11.2	675	PRTS_RAT	P53813 rattus norv
24	165	11.0	1238	JAG2_HUMAN	Q92119 homo sapien
25	165	11.0	1247	JAG2_MOUSE	Q9qy65 mus musculus
26	164	10.9	1202	JAG2_RAT	P97607 rattus norv
27	164	10.9	1429	L112_CAELE	P14585 caenorhabdi
28	164	10.9	2524	NTC3_XENLA	P21783 xenopus lae
29	163.5	10.8	2556	NTC1_HUMAN	P46531 homo sapien
30	163	10.8	644	CD93_MOUSE	Q89103 mus musculus
31	162.5	10.8	2319	NTC3_RAT	Q91172 rattus norv
32	162	10.8	459	PRTS_PIG	Q99122 sus scrofa
33	162	10.8	646	PRTS_FABIT	P98118 oryctolagus

34	162	10.8	833	1	SRC2_MOUSE	P59222 mus musculus
35	162	10.8	870	1	SRC2_HUMAN	Q96gpe homo sapien
36	161	10.7	675	1	PRTS_BOVIN	P07224 bos taurus
37	160.5	10.7	618	1	DLI3_HUMAN	Q9nyj7 homo sapien
38	160.5	10.7	2531	1	NTC1_RAT	Q07008 rattus norv
39	160	10.6	2437	1	NTC1_BRARE	P46530 brachydantio
40	159.5	10.6	643	1	CD93_RAT	Q9et61 rattus norv
41	158.5	10.5	407	1	FA7_BOVIN	P22457 bos taurus
42	158.5	10.5	456	1	PRTS_BOVIN	P00745 bos taurus
43	157.5	10.5	456	1	PRTS_MOUSE	Q9nu41 mus musculus
44	157	10.4	676	1	PRTS_HUMAN	P07225 homo sapien
45	156.5	10.4	1213	1	JAG3_BRARE	Q90y54 brachydantio

ALIGNMENTS

RESULT 1
ID NTC4_MOUSE STANDARD: PRT: 1964 AA.
AC P31655: Q35442: O68314: O68316: Q62389: Q62390: Q9R1M9: Q9R1X0:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
DE [Contains: Transforming protein Int-3].
GN NOTCH4 OR INT3 OR INT-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=92194507; PubMed=1312643;
RA Robbins J., Blondel B.J., Gallahan D., Callahan R.;
RT "Mouse mammary tumor gene int-3: a member of the notch gene family
transforms mammary epithelial cells.";
RL J. Virol. 66:2594-2599(1992).
[2]
RP REVISIONS, SEQUENCE FROM N.A.
RA MEDLINE=97294599; PubMed=9150355;
RX Gallahan D., Callahan R.;
RT "The mouse mammary tumor associated gene INT3 is a unique member of
the NOTCH gene family (NOTCH4).";
RL Oncogene 14:1883-1890(1997).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Testis;
RX MEDLINE=96281668; PubMed=6681805;
RA Uytendaele H., Marazzi G., Wu G., Yan Q., Saasoon D., Kitajewski J.;
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial
cell-specific mammalian Notch gene.";
RL Development 122:2251-2259(1996).
[4]
RP SEQUENCE FROM N.A.
RA Rowen L., Mahapatra G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackone K., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class III
region.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 1436-1600 FROM N.A.
RA MEDLINE=99252212; PubMed=10233982;
RX Lee J.-S., Hartuna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
RT "Intracisternal type A particle-mediated activation of the Notch4/int3
gene in a mouse mammary tumor: generation of truncated Notch4/int3
mRNAs by retroviral splicing events.";
RL J. Virol. 73:5166-5171(1999).
[6]
RP FUNCTION.
RX MEDLINE=21244657; PubMed=11344305;
RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;
RT "Vascular patterning defects associated with expression of activated

RT Notch4 in embryonic endodermium.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648 (2001).
RN [17]
RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
OF VAL-1463.
RX MEDLINE=21523956; PubMed=11518718;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
RT "Murine notch homologs (NL-4) undergo presenilin-dependent
proteolysis.";
RL J. Biol. Chem. 276:40268-40273 (2001).
RN [8]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=1459941;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members.";
RL Func. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (by similarity). May regulate branching
morphogenesis in the developing vascular system.
CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(TEC) which are probably linked by disulfide
bonds.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
kidney, and at lower levels in the ovary and skeletal muscle. A
very low expression is seen in the brain, intestine, liver and
testis.
CC -1- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
embryonic development from 9.0 dpc.
CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(TEC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane.
CC -1- PTM: Phosphorylated.
CC -1- DISEASE: Loss of the extracellular domain causes constitutive
activation of the Notch protein, which leads to hyperproliferation
of glandular epithelial tissues and development of mammary
carcinomas.
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: Contains 29 EGF-like domains.
CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -1- SIMILARITY: Contains 5 ANK repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation-
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC -----
DR EMBL; MG0456; AAB38377.1; -
DR EMBL; U43691; AAC52630.1; -
DR EMBL; U43691; AAC52631.1; -
DR EMBL; AF030001; AAB82004.1; -
DR EMBL; AB016771; BAA32281.1; ALT SEQ.
DR EMBL; AB016772; BAA32283.1; ALT INT.
DR EMBL; AB016773; BAA32284.1; ALT INT.
DR EMBL; AB016774; BAA32285.1; -

DR PIR; T09059; T09059.
DR HSP; P08709; 1BP9.
DR WGD; MG1:107471; Notch4.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-11.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR000800; Notch.
DR Pfam; PF000023; ank; 6.
DR Pfam; PF00008; EGF; 27.
DR Pfam; PF00008; EGF; 27.
DR Pfam; PF00066; notch; 2.
DR PRINTS; PR00010; EGFLOD.
DR PRINTS; PR00011; EGFAMININ.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF CA; 11.
DR SMART; SM00004; NL; 2.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 11.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 21.
DR PROSITE; PS01187; EGF_CA; 9.
KW Receptor; Transcription regulation; Activator; Differentiation;
KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.
FT SIGNAL 1 20
FT CHAIN 21 1964 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.
FT CHAIN 1411 1964 TRANSFORMING PROTEIN INT-3.
FT CHAIN 1428 1964 NOTCH EXTRACELLULAR TRUNCATION.
FT CHAIN 1463 1964 NOTCH INTRACELLULAR DOMAIN.
FT DOMAIN 21 1443 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1444 1464 POTENTIAL.
FT DOMAIN 1465 1964 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 60 EGF-LIKE 1.
FT DOMAIN 61 112 EGF-LIKE 2.
FT DOMAIN 115 152 EGF-LIKE 3.
FT DOMAIN 153 189 EGF-LIKE 4.
FT DOMAIN 191 229 EGF-LIKE 5.
FT DOMAIN 231 271 EGF-LIKE 6.
FT DOMAIN 273 309 EGF-LIKE 7.
FT DOMAIN 311 350 EGF-LIKE 8.
FT DOMAIN 352 388 EGF-LIKE 9.
FT DOMAIN 389 427 EGF-LIKE 10.
FT DOMAIN 429 470 EGF-LIKE 11.
FT DOMAIN 472 508 EGF-LIKE 12.
FT DOMAIN 510 546 EGF-LIKE 13.
FT DOMAIN 548 584 EGF-LIKE 14.
FT DOMAIN 586 622 EGF-LIKE 15.
FT DOMAIN 623 656 EGF-LIKE 16.
FT DOMAIN 658 686 EGF-LIKE 17.
FT DOMAIN 688 724 EGF-LIKE 18.
FT DOMAIN 726 762 EGF-LIKE 19.
FT DOMAIN 764 800 EGF-LIKE 20.
FT DOMAIN 803 839 EGF-LIKE 21.
FT DOMAIN 841 877 EGF-LIKE 22.
FT DOMAIN 878 924 EGF-LIKE 23.
FT DOMAIN 926 962 EGF-LIKE 24.
FT DOMAIN 964 1000 EGF-LIKE 25.
FT DOMAIN 1002 1040 EGF-LIKE 26.
FT DOMAIN 1042 1081 EGF-LIKE 27.
FT DOMAIN 1083 1122 EGF-LIKE 28.
FT DOMAIN 1126 1167 EGF-LIKE 29.
FT REPEAT 1168 1208 LIN/NOTCH 1.
FT REPEAT 1209 1242 LIN/NOTCH 2.
FT REPEAT 1243 1282 LIN/NOTCH 3.
FT REPEAT 1283 1321 ANK 1.
FT REPEAT 1322 1360 ANK 2.
FT REPEAT 1361 1400 ANK 3.
FT REPEAT 1401 1439 ANK 4.
FT REPEAT 1440 1478 ANK 4.
FT REPEAT 1479 1517 ANK 4.
FT REPEAT 1518 1556 ANK 4.
FT REPEAT 1557 1595 ANK 4.
FT REPEAT 1596 1634 ANK 4.
FT REPEAT 1635 1673 ANK 4.
FT REPEAT 1674 1712 ANK 4.
FT REPEAT 1713 1751 ANK 4.
FT REPEAT 1752 1790 ANK 4.

DR SMART, SM00004; NL; 3.
 DR PROSITE; PSS0088; ANK_REPEAT: 5.
 DR PROSITE; PSS0297; ANK_REPEAT: 1.
 DR PROSITE; PSS0010; ASX_HYDROXYL; 11.
 DR PROSITE; PSS0022; EGF_1; 28.
 DR PROSITE; PSS0186; EGF_2; 21.
 DR PROSITE; PSS0187; EGF_CA; 9.
 DR Receptor; Transcription regulation; Activator; Differentiation;
 Developmental protein; Repeat; ANK repeat; EGF-like domain;
 Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 Triplet repeat expansion; Alternative splicing.
 KW SIGNAL
 FT CHAIN 1 23
 FT CHAIN 24 2003
 FT CHAIN 1432 2003
 FT CHAIN 1467 2003
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 FT TRANSMEM 1448 1468
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DR PFam; PF00093; VWC; 2.
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Query Match 12.3%; Score 185; DB 1; Length 816;
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 Matches 47; Conservative 21; Mismatches 64; Indels 28; Gaps 7;

DB 26 PGRVCAVRAGDPVSESFVQRYVPIITT---CGHACACRYRTTYTATRRSGGLAPA 82
 461 PGSEFVCVCKT-GYRIDVYSCTEHDECLTTHNCDEMLAC--FNTV-----G 504
 QY 83 RPRVACCGMWRKTSGLPACGALICOPPCRNCGSCVQGRGRCPAGWRGDTCCQSDVDECS 142
 DB 505 GHNCVCCKRYGTNN-----GTTCAKFKDCGRNGACIAANVACCPGFGFPSCETDIDECSS 560
 QY 143 ARRGCCPQR--CINTAGSYWCQCEGHSLSADGTLCPVKG 180
 DB 561 EGFVQCDSRANCINLPGMYHCECRDGYH---DNMGFAFGG 597

RESULT 4
 FBN2_MOUSE STANDARD; PRT; 2907 AA.

AC O61555; O63957;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 2 precursor.
 GN FBN2 OR FBN-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263670; PubMed=7744963;
 RA Zhang H., Hu W., Ramirez F.,
 RA "Developmental expression of fibrillin genes suggests heterogeneity
 of extracellular microfibrils";
 RL J. Cell Biol. 129:1165-1176(1995).
 RN [2]
 RP SEQUENCE OF 210-317 FROM N.A.
 RX MEDLINE=94140368; PubMed=8307578;
 RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,
 RA Francke U.;
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on
 mouse chromosomes 2 and 18.";
 RL Genomics 18:667-672(1993).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -1- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
 CC -1- SIMILARITY: Contains 47 EGF-like domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 or send an email to license@ebi.ac.uk).

DR EMBL; L39790; AAA74908.1; -;
 DR EMBL; S69359; AAC60685.1; -;
 DR PIR; A57278; A57278.
 DR HSSP; P35555; 1EWN.
 DR MGD; MGI:95490; Fbn2.
 DR GO; GO:0030326; P:limb morphogenesis; IMP.
 DR InterPro; IPR000152; Asx_Hydroxyl.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_1.
 DR InterPro; IPR006209; EGF_1.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00008; EGF; 45.
 DR Pfam; PF00683; TB; 9.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00179; EGF_CA; 43.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 36.
 DR PROSITE; PS01187; EGF_CA; 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
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 FT REPEAT 487 527
 FT DOMAIN 528 567
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FT DISULFID 1696 1710 BY SIMILARITY.

Query Match 12.2%; Score 183.5; DB 1; Length 2907;
Best Local Similarity 23.9%; Pred. No. 2.7e-06;
Matches 60; Conservative 19; Mismatches 85; Indels 87; Gaps 7;

QY 2 RGSQEVLMMLVLAAGTEHAY-----RPRGRVCAVRAHGPVSESFPYQRYVQPLT 54
Db 77 RQQDEILFG---PNVCGSRFHSYCCPGWKTLPGSNQCTVPICRNSCGDGFCSR---PVMC 130
QY 55 TCDGHRACST--YRTIYRTAYRSPFLAPRPRVACCPGMRRTGGLPGACGAALCOPPCR 112
Db 131 TCSSQGISPTGGRKSIQCCSRCMNCGICADHDCCQCKGYIGT-----YCCQPVICENCCQ 185
QY 113 NGGSVQPGRCRCRPAWREGDTCC-----SYDECSARAGGCP-QRCINTAGSIWQCQWE 135
Db 186 NGRGCIIGNRCACVYGFPGQCEBDYRTGPEFTGVNNOMCGQLTGIVCTKLCCATIGR 245
QY 136 -----SVDSCSARAGGCP-QRCINTAGSIWQCQWE 165
Db 246 AMGHCEMCPAOPCPRCRGPFIPIRTGACQDVDECOAIPGLCGGANCINTVGSFEFCRCPA 305
```

QY 166 GHSLADGTLG 176
DB 306 GHKQSETQKC 316

RESULT 5
NEL2_HUMAN STANDARD; PRT; 816 AA.
AC 099435:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-binding protein NELL2 precursor (NEL-like protein 2)
DE (Nel-related protein 2).
OS NELL2 OR NRP2.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97131504; PubMed=8975702;
RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
RT "Cloning and characterization of two novel human cDNAs (NELL1 and
RT NELL2) encoding proteins with six EGF-like repeats.";
RL Genomics 38:273-276 (1996).
RN [2]
RP TSP N-TERMINAL DOMAIN.
RX MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RL J. Mol. Biol. 275:725-730 (1998).
CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 5 WFC domains.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D83018; BAAL1681.1; -
DR HSSP; P00740; 1EDM.
DR Genew; HGNC:7751; NELL2.
DR MIM; 602320; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005508; F:calcium ion binding activity; NAS.
DR GO; GO:0005198; F:structural molecule activity; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR001007; WFC_C.
DR Pfam; PF00008; EGF_5.
DR Pfam; PF02210; TSPN_1.
DR Pfam; PF00093; WVC_3.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00282; LamG_1.
DR SMART; SM00210; TSPN_1.
DR SMART; SM00214; WVC_3.
DR PROSITE; PS00010; Asx_HYDROXYL; 3.

DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WFC_1; 2.
DR PROSITE; PS0184; WFC_2; 3.
KW Glycoprotein; EGF-like domain; Repeat; signal.
FT SIGNAL 1 24
FT CHAIN 25 816
FT DOMAIN 30 258
FT DOMAIN 272 331
FT DOMAIN 332 396
FT DOMAIN 397 439
FT DOMAIN 440 481
FT DOMAIN 482 522
FT DOMAIN 521 553
FT DOMAIN 555 601
FT DOMAIN 602 637
FT DOMAIN 638 693
FT DOMAIN 698 756
FT DOMAIN 758 813
FT DOMAIN 401 413
FT DISULFID 407 422
FT DISULFID 424 438
FT DISULFID 444 457
FT DISULFID 451 466
FT DISULFID 468 480
FT DISULFID 486 499
FT DISULFID 493 508
FT DISULFID 510 521
FT DISULFID 525 535
FT DISULFID 529 541
FT DISULFID 543 552
FT DISULFID 559 572
FT DISULFID 586 591
FT DISULFID 583 600
FT DISULFID 606 619
FT DISULFID 613 628
FT DISULFID 630 636
FT CARBOHYD 53 53
FT CARBOHYD 225 225
FT CARBOHYD 293 293
FT CARBOHYD 298 298
FT CARBOHYD 517 517
FT CARBOHYD 615 615
FT CARBOHYD 635 635
SQ SEQUENCE 816 AA; 91346 MW; 89370B987DC7A324 CRC64;
Query Match 12.1%; Score 182.5; DB 1; Length 816;
Best Local Similarity 37.9%; Pred. No. 8.5e-07;
Matches 36; Conservative 13; Mismatches 37; Indels 9; Gaps 3;
QY 88 CCEGKRTSGLPAGCAALICPPCRNGSCVOPGRCRCPAGKRGTCQSDVDEGARRGG 147
DB 510 CKPGYTGK-----GTTCKAFCKDGCGRNGACIAANVACAPGFTGSCETDIDECSDGFVQ 565
QY 148 CPQR--CINTAGSVWCQCGEHSLSADGTLCPVG 180
DB 566 CDSRANCINLRGWHYCECRDGH--DNGMPSPSG 597
RESULT 6
NEL1_HUMAN STANDARD; PRT; 810 AA.
AC 092832; Q9Y472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1)
DE (Nel-related protein 1).
OS NELL1 OR NRP1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9731504; PubMed=8975702;
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
 Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
 RT "Cloning and characterization of two novel human cDNAs (NEL1 and
 NEL2) encoding proteins with six EGF-like repeats.";
 RL Genomics 38:273-276 (1996).
 RN [2]
 RP SEQUENCE OF 383-810 FROM N.A.
 RA Ting K., Vaetardis H., Mulliken J.B., Bertolami C., Wen Z.,
 RA Young M., Tieu A., Kwong E.;
 RL "Nel" homolog gene expression in craniofacial anomalies.";
 RT Submitted (Sep-1996) to the EMBL/GenBank/DBD databases.
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
 IN POSITIONS 427 AND 771.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D83017; BAA11680.1; -; ALT_FRAME.
 DR EMBL: U57523; AAB06946.1; ALT_FRAME.
 DR HSSP: P07204; IADX.
 DR Genew: HGNC:7750; NEL1.
 DR MIM: 602319; -;
 DR GO: 0007399; P:neurogenesis; TAS.
 DR InterPro: IPR000152; ASX_hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR003129; TSPN.
 DR InterPro: IPR001007; WFC_C.
 DR Pfam: PF00008; EGF_5.
 DR Pfam: PF02210; TSPN; 1.
 DR Pfam: PF00093; WFC_2.
 DR SMART: SM00179; EGF_CA; 2.
 DR SMART: SM00282; LamG; 1.
 DR SMART: SM00210; TSPN; 1.
 DR SMART: SM00214; WFC_3.
 DR PROSITE: PS00010; ASX_HYDROXYL; 3.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 DR PROSITE: PS01208; WFC_1; 2.
 DR PROSITE: PS01208; WFC_2; 2.
 DR GlycoProtein: EGF-like domain; Repeat; Signal.
 KM SIGNAL
 FT CHAIN 1 16
 FT DOMAIN 1 810
 FT DOMAIN 81 230
 FT DOMAIN 271 332
 FT DOMAIN 335 390
 FT DOMAIN 391 433
 FT DOMAIN 434 475
 FT DOMAIN 476 516
 FT DOMAIN 515 547
 FT DOMAIN 548 595
 FT DOMAIN 596 631
 FT DOMAIN 632 687
 FT DOMAIN 692 750
 FT DOMAIN 752 807
 WFC 5.

FT DISULFID 395 407 BY SIMILARITY.
 FT DISULFID 401 416 BY SIMILARITY.
 FT DISULFID 418 432 BY SIMILARITY.
 FT DISULFID 438 451 BY SIMILARITY.
 FT DISULFID 445 460 BY SIMILARITY.
 FT DISULFID 462 474 BY SIMILARITY.
 FT DISULFID 480 493 BY SIMILARITY.
 FT DISULFID 487 502 BY SIMILARITY.
 FT DISULFID 504 515 BY SIMILARITY.
 FT DISULFID 519 529 BY SIMILARITY.
 FT DISULFID 523 535 BY SIMILARITY.
 FT DISULFID 537 546 BY SIMILARITY.
 FT DISULFID 553 566 BY SIMILARITY.
 FT DISULFID 560 575 BY SIMILARITY.
 FT DISULFID 577 594 BY SIMILARITY.
 FT DISULFID 600 613 BY SIMILARITY.
 FT DISULFID 607 622 BY SIMILARITY.
 FT DISULFID 624 630 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 722 732 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 333 383 Y -> D (IN REF. 2).
 FT CONFLICT 573 573 Y -> H (IN REF. 2).
 FT CONFLICT 626 626 S -> C (IN REF. 2).
 SQ SEQUENCE 810 AA; 89606 MW; 549465A9F7AEED0 CRC64;
 Query Match 12.1%; Score 182; DB 1; Length 810;
 Best Local Similarity 37.5%; Pred. No. 9.2e-07;
 Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;
 QY 88 CCRGKRTSGLPAGAGAIICPCGNGSGGQPGRCRCPAGRGDTGSDVDECSARRGG 147
 DB 504 CKPGYVGN---GTCRAFCEBGCRYGTCVAPNKCVPSTGFTGSHCKRIDCESEGIIE 559
 QY 148 C--PQCINTAGSYWCQCEGH---SSADGTLGV 177
 DB 560 CHNHSRCVNLPGWYHCECRSGRHDGTYSLGSESCI 595
 RESULT 7
 ID NEL2 RAT STANDARD; PRT; 816 AA.
 AC 062918;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase C-binding protein NEL2 precursor (NEL-like protein 2).
 OS NEL2 OR NEL.
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=20017976; PubMed=10546494;
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,
 RA Abe T., Matsushashi S., Ting K.;
 RT "Biochemical characterization and expression analysis of neural
 thrombospondin-1-like proteins NEL1 and NEL2.";
 RL Biochem. Biophys. Res. Commun. 265:79-86 (1999).
 RN [2]
 RP TSP N-TERMINAL DOMAIN.
 RX MEDLINE=98153258; PubMed=9480764;

RA Beckmann G., Hanke J., Bork P., Reich J.,
 RT "Meiyang extracellular domains: fold prediction for laminin G-like
 RT and amino-terminal thrombospondin-like modules based on homology to
 RT pentraxins.";
 RL J. Mol. Biol. 275:725-730(1998).
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
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 CC -----
 CC EMBL, U48245; AAC72245.1; -
 CC HSSP; P00740; 1EDM.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; WFC_C.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; WFC; 3.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; WFC; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS01208; WFC_1; 2.
 DR PROSITE; PS01184; WFC_2; 3.
 KW Glycoprotein; EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 816
 FT DOMAIN 30 258
 FT DOMAIN 272 331
 FT DOMAIN 332 396
 FT DOMAIN 397 439
 FT DOMAIN 440 481
 FT DOMAIN 482 522
 FT DOMAIN 521 553
 FT DOMAIN 555 601
 FT DOMAIN 602 637
 FT DOMAIN 638 698
 FT DOMAIN 698 756
 FT DOMAIN 758 813
 FT DISULFID 401 413
 FT DISULFID 407 422
 FT DISULFID 424 438
 FT DISULFID 444 457
 FT DISULFID 451 466
 FT DISULFID 468 480
 FT DISULFID 486 499
 FT DISULFID 493 508
 FT DISULFID 510 521
 FT DISULFID 525 535
 FT DISULFID 529 541
 FT DISULFID 543 552
 FT DISULFID 559 572
 FT DISULFID 566 581
 FT DISULFID 583 600
 FT DISULFID 606 619
 FT DISULFID 613 628
 FT DISULFID 630 636

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 816 AA; 90952 MW; A999F76078060D6B CRC64;
 Query Match 12.0%; Score 180.5; DB 1; Length 816;
 Best Local Similarity 36.8%; Pred. No. 1.2e-06;
 Matches 35; Conservative 14; Mismatches 37; Indels 9; Gaps 3;
 QY 88 CCPGKRTSGLGACGAACICPPCRNGSCVQGRCPAGWRGPTCGSDVEGARRGG 147
 DB 510 CKRPTGN-----GTCCKAFCKGCGNCGACIAANVCAPGPTGPTSCRDIDECSEGFVQ 565
 QY 148 GFOR--CINTAGSYWCQCEGHSLSADGTLCPVKG 180
 DB 566 CDSRANCINLPQWYHCECRDGVH--DNGMFAPGG 597
 RESULT 8
 ID NEIL_RAT STANDARD; PRT; 810 AA.
 AC 062919;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1).
 GN NEIL1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=20017976; PubMed=10548494;
 RA Kuroda S., Oyasu M., Kakakami M., Kanayama N., Tanizawa K., Saito N.,
 RA Abe T., Matsushashi S., Ting K.;
 RT "Biochemical characterization and expression analysis of neural
 RT thrombospondin-1-like proteins NEIL1 and NEIL2.";
 RT Biochem. Biophys. Res. Commun. 265:79-86(1999).
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, U48246; AAC72252.1; -
 CC PIR; T10756; T10756.
 DR HSSP; P35555; 1EWN.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; WFC_C.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; WFC; 2.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00210; TSPN; 1.

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DR SMART: SM00214; VWC: 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WFC 1; 2.
DR PROSITE; PS0184; WFC 2; 2.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 810
FT DOMAIN 81 230
FT DOMAIN 271 332
FT DOMAIN 335 390
FT DOMAIN 391 433
FT DOMAIN 434 475
FT DOMAIN 476 516
FT DOMAIN 515 547
FT DOMAIN 549 595
FT DOMAIN 632 687
FT DOMAIN 692 750
FT DOMAIN 752 807
FT DISULFID 395 407
FT DISULFID 401 416
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FT DISULFID 445 460
FT DISULFID 462 474
FT DISULFID 480 493
FT DISULFID 487 502
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FT DISULFID 600 613
FT DISULFID 607 622
FT DISULFID 624 630
FT CARBOHYD 40 40
FT CARBOHYD 53 53
FT CARBOHYD 83 83
FT CARBOHYD 224 224
FT CARBOHYD 294 294
FT CARBOHYD 372 372
FT CARBOHYD 511 511
FT CARBOHYD 562 562
FT CARBOHYD 609 609
FT CARBOHYD 708 708
SO SEQUENCE 810 AA; 89212 MW; 46F09C466AF9A0B CRC64;

Query Match 12.0%; Score 180; DB 1; Length 810;
Best Local Similarity 36.5%; Pred. No. 1.3e-06;
Matches 35; Conservative 13; Mismatches 38; Indels 10; Gaps 3;

QY 88 CCGMKRTSGLPACCAATCCPPCRNGSCVQGRGRCAGMRGDTCCSDVDECSARRRG 147
DB 504 CCGGIVGN---GTICKAFCEBGRGGCVANRKCVCPSGFGSHCEKDIDCEAFVE 559
QY 148 CP--CRINTAGSYWCQWEGH---SLSDAGTLGV 177
DB 560 CHNYSRCVNLPGWYHCEGRSGFRHDDGTYSLSGSECI 595

RESULT 9.
ID NEL_CHICK STANDARD; PRT; 816 AA.
AC 090827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE NEL_protein precursor (93 kDa protein).

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GN NEL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=90311;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RX MEDLINE=95383734; PubMed=7655083;
RA Matubashi S., Noji S., Koyama E., Miyokai F., Ohuchi H.,
RA Taniguchi S., Hori K.;
RT "New gene, nel, encoding a M(r) 93 k protein with EGF-like repeats is
RT strongly expressed in neural tissues of early stage chick embryos.";
RT Dev. Dyn. 203:212-222 (1995).
RN [2]
RP TSP N-TERMINAL DOMAIN.
RX MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RT J. Mol. Biol. 275:725-730 (1998).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EARLY EMBRYONIC NEURAL
CC TISSUES (BRAIN, SPINAL CORD, DORSAL ROOT GANGLIA); LESS IN OTHER
CC TISSUES SUCH AS CELLS AROUND CARTILAGE, MYOCARDIUM, LUNG
CC MESENCHYMAL CELLS, AND LIVER. AFTER HATCHING EXPRESSION IS
CC RESTRICTED TO NEURAL TISSUES INCLUDING RETINA.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 5 WFC domains.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
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CC EMBL; D86747; BAA13167.1; -.
CC HSSP; P00740; 1EDM.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR00181; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00093; WFC; 3.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00214; WVC; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WFC 1; 2.
DR PROSITE; PS0184; WFC 2; 3.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 25 816
FT DOMAIN 30 258
FT DOMAIN 272 331
FT DOMAIN 332 396
FT DOMAIN 397 439
FT DOMAIN 440 481
FT DOMAIN 482 522
FT DOMAIN 521 553
FT DOMAIN 555 601
FT DOMAIN 602 637

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FT DOMAIN 638 693 VFEC 3.
FT DOMAIN 756 756 VFEC 4.
FT DOMAIN 758 813 VFEC 5.
FT DISULFID 401 413 BY SIMILARITY.
FT DISULFID 407 432 BY SIMILARITY.
FT DISULFID 424 438 BY SIMILARITY.
FT DISULFID 444 457 BY SIMILARITY.
FT DISULFID 451 466 BY SIMILARITY.
FT DISULFID 468 480 BY SIMILARITY.
FT DISULFID 466 499 BY SIMILARITY.
FT DISULFID 493 508 BY SIMILARITY.
FT DISULFID 510 521 BY SIMILARITY.
FT DISULFID 525 535 BY SIMILARITY.
FT DISULFID 529 541 BY SIMILARITY.
FT DISULFID 543 552 BY SIMILARITY.
FT DISULFID 559 572 BY SIMILARITY.
FT DISULFID 566 581 BY SIMILARITY.
FT DISULFID 583 600 BY SIMILARITY.
FT DISULFID 606 619 BY SIMILARITY.
FT DISULFID 613 628 BY SIMILARITY.
FT DISULFID 630 636 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 816 AA, 90968 MW, BPCDBC983C02F831 CR664;

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Query Match 11.7%; Score 176.5; DB 1; Length 816;
Best Local Similarity 39.8%; Pred. No. 2.5e-06;
Matches 33; Conservative 12; Mismatches 33; Indels 5; Gaps 2;

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OY 100 GACGCAICQPPRANGSCVQPCRCPCRMEDTQSDVDECSARRGGCPQ--CINRAG 157
Db 518 GTVCAKAFPCDGCGRNGACIASNVCACPQGTGSPCETIDICSDGTFVQCDSPRANCINPG 577
OY 158 SYWCOCMEGSHLSADGTLCPVPG 180
Db 578 WYHCECRDGYH--DNGMFPBPG 597

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RESULT 10
FBN1_HUMAN STANDARD; PRT; 2871 AA.
AC P35E55;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrillin 1 precursor.
GN FBN1 OR FBN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93372860; PubMed=8364578;
RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
RA Pangilinan T., Bonadio J.;
RT "Genomic organization of the sequence coding for fibrillin, the
RT defective gene product in Marfan syndrome.";
RL Hum. Mol. Genet. 2:961-968(1993).
RN [2]
RP SEQUENCE OF 1-932 FROM N.A.
RC TISSUE=Fibroblast, and Placenta;
RX MEDLINE=94010947; PubMed=7691719;
RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
RT "Fibrillin binds calcium and is coded by cDNAs that reveal a
RT multidomain structure and alternatively spliced exons at the 5'
RT end.";

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RL Genomics 17:476-484(1993).
RN [3]
RP SEQUENCE OF 899-2871 FROM N.A.
RX MEDLINE=91304568; PubMed=1852207;
RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
RT "Partial sequence of a candidate gene for the Marfan syndrome.";
RL Nature 352:334-337(1991).
RN [4]
RP SEQUENCE OF 813-1313 FROM N.A.
RX MEDLINE=91304567; PubMed=1852206;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras P., Ramirez F., Hollister D.W.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RL Nature 352:330-334(1991).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=91317849; PubMed=1860873;
RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;
RT "Purification and partial characterization of fibrillin, a cysteine-
RT rich structural component of connective tissue microfibrils.";
RL J. Biol. Chem. 266:14763-14770(1991).
RN [6]
RP STRUCTURE BY NMR OF 2054-2125.
RX MEDLINE=98031893; PubMed=9362480;
RA Yuan X., Downing A.K., Knott V., Handford P.A.;
RT "Solution structure of the transforming growth factor beta-binding
RT protein-like module, a domain associated with matrix fibrils.";
RL EMBO J. 16:6659-6666(1997).
RN [7]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96144829; PubMed=8568869;
RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
RT "Calcium binding properties of an epidermal growth factor-like domain
RT pair from human fibrillin-1.";
RL J. Mol. Biol. 255:22-27(1996).
RN [8]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96222301; PubMed=8653794;
RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
RA Handford P.A.;
RT "Solution structure of a pair of calcium-binding epidermal growth
RT factor-like domains: implications for the Marfan syndrome and other
RT genetic disorders.";
RL Cell 85:597-605(1996).
RN [9]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=96174615; PubMed=8594563;
RA Collod G., Beroud C., Soussi T., Junien C., Boileau C.;
RT "Software and database for the analysis of mutations in the human
RT FBN1 gene.";
RL Nucleic Acids Res. 24:137-141(1996).
RN [10]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=97169383; PubMed=9016526;
RA Collod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
RA Richards R.I., Wang W., Junien C., Boileau C.;
RT "Marfan Database (second edition): software and database for the
RT analysis of mutations in the human FBN1 gene.";
RL Nucleic Acids Res. 25:147-150(1997).
RN [11]
RP REVIEW ON VARIANTS.
RX MEDLINE=98062175; PubMed=9401003;
RA Hayward C., Brock D.J.H.;
RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
RT fibrillogenopathies.";
RL Hum. Mutat. 10:415-423(1997).
RN [12]
RP VARIANT MFS PRO-1137.
RX MEDLINE=91304569; PubMed=1852208;
RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.;

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RA Curristin S.M., Stetren G., Meyers D.A., Francomano C.A.;
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in
 the fibrillin gene.";
 RL Nature 352:337-339(1991).
 RN [13]
 RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.
 RX MEDLINE=93250834; PubMed=1301946;
 RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome
 patients at cysteine residues in EGF-like domains.";
 RL Hum. Mutat. 1:366-374(1992).
 RN [14]
 RP VARIANT MFS SER-2307.
 RX MEDLINE=92235290; PubMed=1569206;
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
 Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
 RT "Marfan phenotype variability in a family segregating a missense
 mutation in the epidermal growth factor-like motif of the fibrillin
 gene.";
 RL J. Clin. Invest. 89:1674-1680(1992).
 RN [15]
 RP VARIANTS MFS IIE-548 AND ALA-723.
 RX MEDLINE=94010946; PubMed=8406497;
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
 Pyeritz R.E., Francomano C.A.;
 RT "Four novel FBN1 mutations: significance for mutant transcript level
 and EGF-like domain calcium binding in the pathogenesis of Marfan
 syndrome.";
 RL Genomics 17:468-475(1993).
 RN [16]
 RP VARIANTS MFS SER-2144.
 RX MEDLINE=93278402; PubMed=8504310;
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 disrupt calcium binding of the epidermal growth factor-like module.";
 RL Hum. Mol. Genet. 2:475-477(1993).
 RN [17]
 RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
 RP ALA-1148.
 RX MEDLINE=94108431; PubMed=8281141;
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gaesner C.,
 Berg M.A., Miller D.C., Francke U.;
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 of five new mutations, including two in 8-cysteine domains.";
 RL Hum. Mol. Genet. 2:1813-1821(1993).
 RN [18]
 RP VARIANTS MFS GLY-217 AND ARG-2627.
 RX MEDLINE=95067970; PubMed=7977366;
 RA Karttunen L., Ragnunath M., Loenqvist L., Peltonen L.;
 RT "A compound-heterozygous Marfan patient: two defective fibrillin
 alleles result in a lethal phenotype.";
 RL Am. J. Hum. Genet. 55:1083-1091(1994).
 RN [19]
 RP VARIANT EL LYS-2447.
 RX MEDLINE=94245249; PubMed=8188302;
 RA Lonnqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 Peltonen L.;
 RT "A novel mutation of the fibrillin gene causing ectopia lentis.";
 RL Genomics 19:573-576(1994).
 RN [20]
 RP VARIANT MFS CYS-627.
 RX MEDLINE=94272487; PubMed=8004112;
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains
 of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
 syndrome patients.";
 RL Hum. Mol. Genet. 3:373-375(1994).
 RN [21]
 RP VARIANT MFS CYS-122.
 RX MEDLINE=94314977; PubMed=8040326;
 RA Stahl-Hallengren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 Saxne T., Tornqvist K., Peltonen L.;
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth

RT factor-like motifs of the FBN1 polypeptide is connected to a novel
 RT variant of Marfan syndrome.";
 RL J. Clin. Invest. 94:709-713(1994).
 RN [22]
 RP VARIANT MFS TYR-1223.
 RX MEDLINE=94351682; PubMed=8071963;
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
 RT "A new missense mutation of fibrillin in a patient with Marfan
 syndrome.";
 RL J. Med. Genet. 31:338-339(1994).
 RN [23]
 RP VARIANT MFS HIS-1170.
 RX MEDLINE=95174777; PubMed=7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 arachnodactyly.";
 RL Mol. Cell. Probes 8:325-327(1994).
 RN [24]
 RP VARIANTS MFS GLY-217; ASN-1023; ARG-1074; TYR-1242; ARG-1513;
 RP GLU-2127; TRP-2151; LYS-2447 AND ARG-2511.
 RX MEDLINE=94184368; PubMed=8136837;
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 lentis and neonatal Marfan syndrome.";
 RL Nat. Genet. 6:64-69(1994).
 RN [25]
 Query Match 11.7%; Score 176.5; DB 1; Length 2871;
 Best Local Similarity 22.7%; Pred. No. 9.1e-06;
 Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;
 QY 26 PGRRCVAVRAGDPPSESVQVRYQPFLLTCDGHR---ACSTYRTIYRAYSFGLAPA 82
 DB 75 PGAGNCIVPIGRHSGDGFCSR---PNNCTPSSQIAPSCS-RSICNIRCMNGSGCS 130
 QY 83 RPRVACBPGRKTSGLPGACCAAIQPPRCNGSCVQGRRCRCPAGMGDTQ----- 135
 DB 131 DDHCLCQGVYIGTH-----CGQPVCESSGLNGRCVARNRCACVYGFPGQCDERYRTGP 185
 QY 136 -----S 136
 DB 186 CFTVISNMCGQQLSGIVCTKQLCCATVGRAMGHCPCPAQPHRCRRGFIPIRTGACQ 245
 QY 137 DVDECSARAGGCP-ORCINTAGSYWCQCEGHSLSADTLG-----VPKGG--- 181
 DB 246 DVDECGALPGLCGGGNCINTVGSFPCCKPAGHKLNKNSQKEDIDECSTIGICEGGECT 305
 QY 182 -----PPRVAVPNTG 191
 DB 306 NTVSSYFCKCPGFGYTSBDG 325
 RESULT 11
 NTC3_HUMAN
 ID NTC3_HUMAN STANDARD; PRT; 2321 AA.
 AC Q9UM47; Q9UEB3; Q9UPL3; Q9Y6L8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).
 GN NOTCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8878478;
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,
 Alanowitch S., Domenga V., Cecillon M., Marechal E., Maciazek J.,
 Vaysiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissbach J.,
 Bach J.-F., Bousse M.-G., Tournier-Lasserre E.;
 RT "Notch3 mutations in CADASIL, a hereditary adult-onset condition

RT causing stroke and dementia." ;
 RL Nature 383:707-710 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gunel M., Artavanis-Tsakonas S.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lamerding J.E., McCready P.M., Skowronski E., Adamson A.W.,
 RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilaasen S.,
 RA Phan H., Velasco N., Gaines J., Dargahan L., Poundstone P.,
 RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
 RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
 RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,
 RA Carrano A.V.;
 RL "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in
 19p13.1." ;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141;
 RP ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212;
 RP GLY-222; TYR-224; CYS-258; TYR-542; CYS-558; CYS-578; CYS-726;
 RP ARG-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS
 RP ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.
 RX MEDLINE=98049753; PubMed=938839;
 RA Joutel A., Vahedi K., Corpechot C., Troesch A., Chabrier H.,
 RA Vaysiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,
 RA Bach J.-F., Tourner-Lasserre E.;
 RL "Strong clustering and stereotyped nature of Notch3 mutations in
 CADASIL patients." ;
 RL Lancet 350:1511-1515 (1997).
 RN [5]
 RP VARIANT CADASIL 114-GLY--PRO-120 DEL.
 RX MEDLINE=2026473; PubMed=10802807;
 RA Joutel A., Chabrier H., Vahedi K., Domenga V., Vaysiere C.,
 RA Ruchoux M.M., Lucas C., Lays D., Bousser M.-G., Tourner-Lasserre E.;
 RL "Splice site mutation causing a seven amino acid Notch3 in-frame
 deletion in CADASIL." ;
 RL Neurology 54:1874-1875 (2000).
 RN IDENTIFICATION OF LIGANDS.
 RX MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcanguin M.-L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RL Am. J. Pathol. 154:785-794 (1999).
 RL [6]
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (By similarity).
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult
 CC tissues.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -1- PTM: Phosphorylated (By similarity).

CC -1- DISEASE: Defects in NOTCH3 are associated with CADASIL (cerebral
 CC autosomal dominant arteriopathy with subcortical infarcts and
 CC leukoencephalopathy) which causes a type of stroke and dementia of
 CC which key features include recurrent subcortical ischemic events
 CC and vascular dementia.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: Contains 34 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -1- SIMILARITY: Contains 5 ANK repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL, U97669; AAB91371.1; -.
 CC DR EMBL, AF058900; AAC14346.1; -.
 CC DR EMBL, AF058881; AAC14346.1; JOINED.
 CC DR EMBL, AF058882; AAC14346.1; JOINED.
 CC DR EMBL, AF058883; AAC14346.1; JOINED.
 CC DR EMBL, AF058884; AAC14346.1; JOINED.
 CC DR EMBL, AF058885; AAC14346.1; JOINED.
 CC DR EMBL, AF058886; AAC14346.1; JOINED.
 CC DR EMBL, AF058887; AAC14346.1; JOINED.
 CC DR EMBL, AF058888; AAC14346.1; JOINED.
 CC DR EMBL, AF058889; AAC14346.1; JOINED.
 CC DR EMBL, AF058890; AAC14346.1; JOINED.
 CC DR EMBL, AF058891; AAC14346.1; JOINED.
 CC DR EMBL, AF058892; AAC14346.1; JOINED.
 CC DR EMBL, AF058893; AAC14346.1; JOINED.
 CC DR EMBL, AF058894; AAC14346.1; JOINED.
 CC DR EMBL, AF058895; AAC14346.1; JOINED.
 CC DR EMBL, AF058896; AAC14346.1; JOINED.
 CC DR EMBL, AF058897; AAC14346.1; JOINED.
 CC DR EMBL, AF058898; AAC14346.1; JOINED.
 CC DR EMBL, AF058899; AAC14346.1; JOINED.
 CC DR EMBL, AC004257; AAC04897.1; -.
 CC DR EMBL, AC004663; AAC15789.1; ALT_INIT.
 CC DR PIR, S78549; S78549.
 CC DR HSSP, P00740; 1EDM.
 CC DR GENE, HGNC:7883; NOTCH3.
 CC DR MIM, 600276; -.
 CC DR MIM, 125310; -.
 CC DR InterPro: IPR002110; ANK.
 CC DR InterPro: IPR000152; Asx_hydroxy1.
 CC DR InterPro: IPR000742; EGF_2.
 CC DR InterPro: IPR001881; EGF_Ca.
 CC DR InterPro: IPR001438; EGF_11.
 CC DR InterPro: IPR006209; EGF_like.
 CC DR InterPro: IPR002049; LamInn_EGF.
 CC DR InterPro: IPR000800; Notch.
 CC DR Pfam: PF00023; ank; 6.
 CC DR Pfam: PF00008; EGF; 34.
 CC DR Pfam: PF00066; notch; 3.
 CC DR PRINTS: PR00010; EGFBLD.
 CC DR PRINTS: PR00011; EGFBLD.
 CC DR PRINTS: PR01452; NOTCH.
 CC DR SMART, SM00248; ANK; 6.
 CC DR SMART, SM00179; EGF_CA; 19.
 CC DR PROSITE, PS00088; ANK_REPEAT; 4.
 CC DR PROSITE, PS0297; ANK_REPEAT; 1.
 CC DR PROSITE, PS00010; ASX_HYDROXYL; 18.
 CC DR PROSITE, PS00022; EGF_1; 33.
 CC DR PROSITE, PS01186; EGF_2; 25.
 CC DR PROSITE, PS01187; EGF_CA; 16.
 CC KW Receptor; Transcription regulation; Activator; Differentiation;
 CC Developmental protein; Repeat; ANK repeat; EGF-like domain;
 CC Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 CC Disease mutation.
 CC KW

RX MEDLINE=99192777; PubMed=10092817;
 RA Nepomceno R.R., Ruiz S., Park M., Tenner A.J.;
 RT "C1qR is a heavily O-glycosylated cell surface protein involved in
 RL the regulation of phagocytic activity.";
 RL J. Immunol. 162:3583-3589 (1999).
 CC -1- FUNCTION: Receptor (or element of a larger receptor complex) for
 CC C1q, mannose-binding lectin (MBL) and pulmonary surfactant
 CC protein A (SPA). May mediate the enhancement of phagocytosis in
 CC monocytes and macrophages upon interaction with soluble defense
 CC collagens. May play a role in intercellular adhesion.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
 CC platelets, cells of myeloid origin, such as monocytes and
 CC neutrophils. Not expressed in cells of lymphoid origin.
 CC -1- PM: N- and O-glycosylated.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -1- SIMILARITY: Contains 5 EGF-like domains.
 CC -1- CAUTION: Has been sometimes referred to as a collectin receptor.
 CC -1- CAUTION: According to Ref.5, C1q is not a ligand for C1qR1.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 3.1.6(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456_g.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U94333; AAB53110.1; -;
 DR EMBL; AL118508; CAC00597.1; -;
 DR EMBL; BC028075; AAH28075.1; -;
 DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:15855; C1QR1.
 DR MIM; 120577; -;
 DR GO; GO:0016021; C:integral to membrane; IC.
 DR GO; GO:0004872; F:receptor activity; NAS.
 DR GO; GO:0016337; P:cell-cell adhesion; IDA.
 DR GO; GO:0042116; P:macrophage activation; NAS.
 DR GO; GO:0006909; P:phagocytosis; NAS.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00008; EGF_5.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Pfam; PF01108; Tissue_fac; 1.
 DR SMART; SMO0034; CLECT_1.
 DR SMART; SMO0179; EGF_Ca; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_Ca; 3.
 KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 1 21
 FT DOMAIN 22 652 COMPLEMENT COMPONENT C1Q RECEPTOR.
 FT DOMAIN 24 580 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 581 601 POTENTIAL.
 FT DOMAIN 602 652 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 174 C-TYPE LECTIN.
 FT DOMAIN 260 301 EGF-LIKE 1.
 FT DOMAIN 302 344 EGF-LIKE 2.
 FT DOMAIN 345 384 EGF-LIKE 3.
 FT DOMAIN 385 426 EGF-LIKE 4.
 FT DOMAIN 427 468 EGF-LIKE 5.
 FT DOMAIN 594 601 POLY-LEU.
 FT DISULFID 264 275 BY SIMILARITY.
 FT DISULFID 271 285 BY SIMILARITY.
 FT DISULFID 287 300 BY SIMILARITY.
 FT DISULFID 306 317 BY SIMILARITY.

FT DISULFID 311 328 BY SIMILARITY.
 FT DISULFID 330 343 BY SIMILARITY.
 FT DISULFID 349 358 BY SIMILARITY.
 FT DISULFID 354 363 BY SIMILARITY.
 FT DISULFID 369 387 BY SIMILARITY.
 FT DISULFID 389 400 BY SIMILARITY.
 FT DISULFID 396 409 BY SIMILARITY.
 FT DISULFID 411 425 BY SIMILARITY.
 FT DISULFID 431 443 BY SIMILARITY.
 FT DISULFID 439 452 BY SIMILARITY.
 FT DISULFID 454 467 BY SIMILARITY.
 FT CAROHRD 325 325 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 318 318 V -> A.
 FT CONFLICT 22 22 /FTID=VAR 013573.
 FT CONFLICT 36 36 T -> V (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 38 39 C -> T (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 155 155 TA -> RT (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 155 155 S -> N (IN REF. 1).
 FT CONFLICT 186 186 G -> A (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 492 492 S -> A (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 496 496 R -> Q (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 504 504 R -> G (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 541 541 P -> S (IN REF. 1).
 SQ SEQUENCE 652 AA; 68560 MW; EECARQFEAC55FCAC2 CRC64;
 Query Match 11.6%; Score 175; DB 1; Length 652;
 Best Local Similarity 33.1%; Pred. No. 2.6e-06;
 Matches 60; Conservative 10; Mismatches 57; Indels 54; Gaps 13;
 QY 25 RPRRRV-----CAVRAHGPVSESFYQVYQVFLTTCDGHRACSTYRTVYTAVRASPG 78
 DB 288 RPPRLDDLVTCASR---NPCSSS-----PCRGATCV----- 318
 QY 79 LAPARPRYAC-CP-GMRTSGLPACGALIQ-PPCRNGSGCVQ-PG--RCRCPAGMR-- 130
 DB 319 LGPHKNTYTCRCPOGYQDSSQLDCVDVDEQDSCAC--BCVTPGGFRCECWGYEPG 376
 QY 131 --GPTQSDVVECSARRGCGCPORCINTAGSYWCQCEGHSLSA-DGTL-----CVPKGG 181
 DB 377 GPGEACQDVDECALGRSPCAQCGTNTGDSHCSEBSYIVLAGEGTGCGQDVDECVGPG 436
 QY 182 P 182
 DB 437 P 437
 RESULT 13
 NOTC DROME STANDARD; PRT; 2703 AA.
 AC P07207; O97458; P04154; Q9W4T8;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neogenetic locus Notch protein precursor.
 GN N OR EG:140G11.1 OR EG:163A10.2 OR CG33936.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=86079539; PubMed=3935325;
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neogenetic locus notch implies a gene
 RT product that shares homology with proteins containing EGF-like
 RT repeats.";
 RL Cell 43:567-581 (1985).
 RN [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=Canton-S; and Oregon-R; TISSUE=Embryo;
 RX MEDLINE=87064624; PubMed=3097517;

RA Kidd S., Kelley M.R., Young M.W.;
 RT "Sequence of the notch locus of *Drosophila melanogaster*: relationship
 of the encoded protein to mammalian clotting and growth factors."; Mol.
 Cell. Biol. 6:3094-3108(1986).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 Abul J.F., Agbayani A., An H.-U., Andrews-Frankoch C., Baldwin D.,
 Balow R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durkin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny J., Moshrefi A.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paetle J.M.,
 Palczolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."; Science
 287:2185-2195(2000).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Oregon-R;
 RC MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Galt M.X., Ashburner M., Murphy L., Harris D.,
 Barrell B.G., Ferraz C., Vidal S., Brun C., Demilles J., Cadieu E.,
 Dreano S., Gloux S., Leleure V., Mottier S., Galibert F., Botkova D.,
 Minna B., Kataros F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 Papadogiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 Papadogiannakis G., Peter A., Schoettler P., Wener M., Mourikios F.,
 Beilner N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
 Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
 McMillan P.J., Sales C., Tait E.A., Valenti P., Saunders R.D.C.,
 Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of *D.*
melanogaster."; Science 287:2220-2222(2000).
 [5]
 RN SEQUENCE OF 2505-2611 FROM N.A.
 RP MEDLINE=8509329; PubMed=2961631;
 RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
 RT "Opa: a novel family of transcribed repeats shared by the Notch locus
 and other developmentally regulated loci in *D. melanogaster*."; Cell
 40:55-62(1985).
 [6]
 RN *SEQUENCE OF 1-8 FROM N.A.
 RP MEDLINE=87257846; PubMed=3037327;

RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
 RT "Restriction of P-element insertions at the Notch locus of *Drosophila*
melanogaster."; Mol. Cell. Biol. 7:1545-1548(1987).
 [7]
 RN REVIEW.
 RP Harris M.A.;
 RT "Many cell types specified by Notch function."; Curr. Biol.
 11:120-122(1991).
 RL -1- FUNCTION: Functions as a receptor for membrane-bound ligands Delta
 and Serrate to regulate cell-fate determination. Upon ligand
 activation through the released notch intracellular domain (NICD)
 it forms a transcriptional activator complex with Su(H)
 (Suppressor of hairless) and activates genes of the enhancer of
 split locus. Essential for proper differentiation of ectoderm.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: Contains 36 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -1- SIMILARITY: Contains 6 ANK repeats.
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 CC -----
 DR EMBL: M16152; AAB59220.1; -;
 DR EMBL: M16153; AAB59220.1; JOINED.
 DR EMBL: M16149; AAB59220.1; JOINED.
 DR EMBL: M16150; AAB59220.1; JOINED.
 DR EMBL: M16151; AAB59220.1; JOINED.
 DR EMBL: M13689; AAA28725.1; -;
 DR EMBL: M13689; AAA28725.1; JOINED.
 DR EMBL: K03507; AAA28725.1; JOINED.
 DR EMBL: AE003426; AAF45848.2; -;
 DR EMBL: AL035395; CAB37610.1; JOINED.
 DR EMBL: M12175; AAA74496.1; -;
 DR EMBL: M16025; AAA28726.1; -;
 DR PIR: A24420; A24420.
 DR HSSD: P00740; 1EDM.
 DR FlyBase: FBgn0004647; N.
 DR GO: GO:0005634; C:nucleus; NAS.
 DR GO: GO:0005886; C:plasma membrane; IDA.
 DR GO: GO:0004888; F:transmembrane receptor activity; NAS.
 DR GO: GO:0007403; P:determination of glial fate; IMP.
 DR GO: GO:0007293; P:egg chamber formation; IMP.
 DR GO: GO:0042067; P:establishment of committal polarity (sensu. . .); NAS.
 DR GO: GO:0046331; P:lateral inhibition; NAS.
 DR GO: GO:0007498; P:mesoderm development; IMP.
 DR GO: GO:0007519; P:myogenesis; IMP.
 DR GO: GO:0046329; P:negative regulation of JNK cascade; NAS.
 DR GO: GO:0045465; P:R8 differentiation; NAS.
 DR GO: GO:0045468; P:regulation of R8 spacing; NAS.
 DR GO: GO:0007423; P:sensory organ development; IMP.
 DR GO: GO:0007424; P:tracheal system development (sensu Insecta); NAS.
 DR GO: GO:0007476; P:wing morphogenesis; NAS.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_T1.
 DR InterPro: IPR006209; EGF_T1.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00023; ank; 7.
 DR Pfam: PF00008; EGF; 36.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFBL00D.
 DR PRINTS: PR00011; EGFBLMININ.


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DR PRINTS; PRO1452; NOTCH.
DR SMART; SM00248; ANK; 7.
DR SMART; SM00179; EGF CA; 24.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00068; ANK_REPEAT; 5.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF 1; 34.
DR PROSITE; PS01186; EGF 2; 28.
DR PROSITE; PS01187; EGF CA; 21.
DR Receptor; Transcription regulation; Activator; Differentiation;
KW Developmental protein; Neurogenesis; Repeat; ANK repeat;
KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 44
FT CHAIN 1 2703
FT DOMAIN 45 1745
FT TRANSMEM 1746 1766
FT DOMAIN 1767 2703
FT DOMAIN 58 95
FT DOMAIN 96 136
FT DOMAIN 139 176
FT DOMAIN 177 215
FT DOMAIN 217 253
FT DOMAIN 255 291
FT DOMAIN 293 329
FT DOMAIN 331 370
FT DOMAIN 372 408
FT DOMAIN 409 447
FT DOMAIN 449 486
Query Match 11.6%; Score 175; DB 1; Length 2703;
Beat Local Similarity 25.3%; Pred. No. 1.1e-05;
Matches 57; Conservative 22; Mismatches 62; Indels 84; Gaps 13;

OY 18 GSTEHAHPRRVCVRAH--GDVSESFVQVYQFPLTCDGHRACSTYRT---IYRT 71
DB 70 GGTCTVQLNGKTYCACHSYVD-----YCHRNPCNSMRCNGSTQY 113
OY 72 AYRSPGLAPAPRRAC--CP-GMKRT---SGLRGACGALC----- 107
DB 114 TFRN-----GRPGISCKCPFLDSLCIAPNACDHVTCINGTQCKLEETCA 167
OY 108 -----QPPCRNGSCV-----QPRCRCPAGWRGDTCCSDVDECSA---R 144
DB 168 NGYTERGETKNLCASSPCRNATCTALAGSSSFCSCPGPTGTCGYDIECCSNCK 227
OY 145 RGGCPQRCINTAGSYWCQCBGSHLSADGTLCPVKGPPRAVNP 189
DB 228 YGG--TCVNTHGSYQCMCPTGYT-----GKDCDTYKRP--CSPSP 263

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RP SEQUENCE FROM N.A.
RX MEDLINE=96044428; PubMed=7557988;
RA Zimmermann K., Holschen S., Hafner M., Nischt R.;
RT "Genomic sequences and structural organization of the human nidogen
RL gene (NID).";
RL Genomics 27:245-250(1995).
RP [3]
RP SEQUENCE OF 667-1247 FROM N.A.
RX TISSUE=Placenta;
RA MEDLINE=89270475; PubMed=2471408;
RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,
RA Timpi R., Chu M.L., Uitto J.;
RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the
RT gene to chromosome 14q31.";
RT Am. J. Hum. Genet. 44:876-885(1989).
CC -1- FUNCTION: SUPPATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN
CC BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ.
CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-
CC EXTRACELLULAR MATRIX INTERACTIONS.
CC -1- SUBUNIT: Interacts with FBIN1 (By similarity).
CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC -1- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
CC -1- SIMILARITY: Contains 5 LDL-receptor YWTD domains.
CC -----
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CC -----
DR EMBL; M30269; AAF5932.1; -
DR EMBL; X82245; CAAS7709.1; JOINED.
DR EMBL; X84819; CAAS7709.1; JOINED.
DR EMBL; X84820; CAAS7709.1; JOINED.
DR EMBL; X84821; CAAS7709.1; JOINED.
DR EMBL; X84822; CAAS7709.1; JOINED.
DR EMBL; X84823; CAAS7709.1; JOINED.
DR EMBL; X84824; CAAS7709.1; JOINED.
DR EMBL; X84825; CAAS7709.1; JOINED.
DR EMBL; X84826; CAAS7709.1; JOINED.
DR EMBL; X84827; CAAS7709.1; JOINED.
DR EMBL; X84828; CAAS7709.1; JOINED.
DR EMBL; X84829; CAAS7709.1; JOINED.
DR EMBL; X84830; CAAS7709.1; JOINED.
DR EMBL; X84831; CAAS7709.1; JOINED.
DR EMBL; X84832; CAAS7709.1; JOINED.
DR EMBL; X84833; CAAS7709.1; JOINED.
DR EMBL; X84834; CAAS7709.1; JOINED.
DR EMBL; X84835; CAAS7709.1; JOINED.
DR EMBL; X84836; CAAS7709.1; JOINED.
DR EMBL; X84837; CAAS7709.1; JOINED.
DR EMBL; M27445; AAF57261.1; -
DR PIR; A33322; MATHND.
DR PDB; 1NDX; 29-DEC-99.
DR Genew; HGNC:7821; NID.
DR MIM; 131390; -
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006605; GZF.
DR InterPro; IPR000033; LDL receptor rep.
DR InterPro; IPR003886; Nidogen ext.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF00058; Idl_recept b; 3.
DR Pfam; PF00086; thyroglobulin_1; 1.
DR SMART; SM00179; EGF CA; 2.
DR SMART; SM00682; GZF; 1.
DR SMART; SM00135; LY; 5.

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DR SMART; SM00539; NIDO; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 2.
DR Basament membrane; Extracellular matrix; Glycoprotein; Sulfation;
KW Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion;
KM 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 1247
FT DOMAIN 29 669
FT DOMAIN 670 917
FT DOMAIN 918 1247
FT DOMAIN 386 426
FT DOMAIN 668 709
FT DOMAIN 710 751
FT DOMAIN 758 801
FT DOMAIN 802 840
FT DOMAIN 872 919
FT DOMAIN 989 1030
FT DOMAIN 1032 1073
FT DOMAIN 1075 1118
FT DOMAIN 1124 1163
FT DOMAIN 1208 1244
FT MOD RES 289 289
FT MOD RES 296 296
FT MOD RES 672 672
FT DISULFID 679 695
FT DISULFID 697 708
FT DISULFID 714 727
FT DISULFID 721 736
FT DISULFID 738 750
FT DISULFID 762 777
FT DISULFID 769 787
FT DISULFID 789 800
FT DISULFID 806 817
FT DISULFID 811 826
FT DISULFID 828 839
FT DISULFID 1212 1233
FT DISULFID 1219 1232
FT DISULFID 1234 1243
FT SITE 702 704
FT SITE 1137 1137
FT CARBOHYD 33 34
FT CONFLICT 37 42
FT CONFLICT 115 115
FT CONFLICT 1247 AA; 136488 MW; 46815B3CEC1575B CRC64;
SQ SEQUENCE 115 115
Query Match 11.5%; Score 173.5; DB 1; Length 1247;
Best Local Similarity 25.8%; Pred. No. 6.6e-06;
Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;
QY 20 THAIRPRGRV-----CAVRANG-----DPVSEFVQRYVQPLPTTCGHRACSTYR 66
DB 681 TNAACRPGRPTQFTCECSIGFRGDGRTCYDIECE-----QP--SVCSHTICNNH- 730
QY 67 TYRTAYRSPGLAPRPRVACCPGKRTSGPAGCAIACP--CRNG----- 114
DB 731 -----DETFRCEVEGQPSD--EGTCAVAVDPRPYNVCEGLHNCIDIPOR 774
QY 115 GSCVPG-----RCRCPAGWRGD--TCQSDVDECSARRGCGPCPCINTAGSYCCQMEGHS 168
DB 775 AGCIYTGSSSYTCSCLPGSPSGQACQ--DVDECQSRCHPDAPFCVNTGSGFTCCCKPCY- 832
QY 169 LSADGLTCLP-----KGPFRVAENPTG----- 191
DB 833 -QGDFRCVPGVEVETRCQREHILGAAGATDPORPIPGHVPEDCAHGHVAPTCQGH 891
QY 192 -----VDSAMKEEYORLOSRLDLEELQVLPLH-SLASQMLEHGLDPRGSLVHS 243
DB 892 STGYCWCVDROGR-EVEGRTIRPKMTPPCLSTVAPRPIHOGPAVPTAVIPLP-PGTHLL-- 947

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QY 244 FOGLRINDL 253
DB 948 FAOTGKIERYL 957
RESULT 15
FBN1_MOUSE STANDARD; PRT; 2871 AA.
ID FBN1_MOUSE Q61554; Q60826;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrillin-1 precursor.
GN FBN1 OR FBN-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95130561; PubMed=7829516;
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Panglilian T.,
RA Pereira L., Ramirez F., Bonadio J.;
RT "Primary structure and developmental expression of Fbn-1, the mouse
RT fibrillin gene.";
RL J Biol. Chem. 270:1798-1806(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Mada J., Liu Z., Kanwar Y.S.;
RA Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.
RL
CC -! FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
CC -! FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
CC MICROFIBRILS (BY SIMILARITY).
CC -! SIMILARITY: Contains 47 EGF-like domains.
CC -! SIMILARITY: Contains 7 TGF-beta binding protein (TGFBRP) domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29454; AAA56840.1; -
DR EMBL; U22493; AAA64217.1; -
DR PIR; A55624; A55624.
DR HSSP; P35551; IABJ.
DR MGD; MGI:95489; Fbn1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002212; Fibrill-1-assoc.
DR Pfam; PF00008; EGF; 46.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS01187; EGF_CA; 43.
DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW Repeat; Signal; Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 2871
FT DOMAIN 81 112
FT DOMAIN 115 146
FT DOMAIN 147 178
FT DOMAIN 246 287
FT DOMAIN EGF-LIKE 4, CALCIUM-BINDING.

```

FT	DOMAIN	288	329	EGF-LIKE 5, CALCIUM-BINDING.
FT	DOMAIN	330	401	TGFBP 1.
FT	DOMAIN	402	446	PRO-RICH.
FT	DOMAIN	449	489	EGF-LIKE 6.
FT	DOMAIN	490	529	EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	530	571	EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	572	612	EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	613	653	EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	656	721	TGFBP 2.
FT	DOMAIN	723	764	EGF-LIKE 11, CALCIUM-BINDING.
FT	DOMAIN	765	806	EGF-LIKE 12, CALCIUM-BINDING.
FT	DOMAIN	807	846	EGF-LIKE 13, CALCIUM-BINDING.
FT	DOMAIN	910	951	EGF-LIKE 14, CALCIUM-BINDING.
FT	DOMAIN	952	1018	TGFBP 3.
FT	DOMAIN	1028	1069	EGF-LIKE 15, CALCIUM-BINDING.
FT	DOMAIN	1070	1112	EGF-LIKE 16, CALCIUM-BINDING.
FT	DOMAIN	1113	1154	EGF-LIKE 17, CALCIUM-BINDING.
FT	DOMAIN	1155	1196	EGF-LIKE 18, CALCIUM-BINDING.
FT	DOMAIN	1197	1237	EGF-LIKE 19, CALCIUM-BINDING.
FT	DOMAIN	1238	1279	EGF-LIKE 20, CALCIUM-BINDING.
FT	DOMAIN	1280	1321	EGF-LIKE 21, CALCIUM-BINDING.
FT	DOMAIN	1322	1362	EGF-LIKE 22, CALCIUM-BINDING.
FT	DOMAIN	1363	1403	EGF-LIKE 23, CALCIUM-BINDING.
FT	DOMAIN	1404	1445	EGF-LIKE 24, CALCIUM-BINDING.
FT	DOMAIN	1446	1486	EGF-LIKE 25, CALCIUM-BINDING.
FT	DOMAIN	1487	1527	EGF-LIKE 26, CALCIUM-BINDING.
FT	DOMAIN	1528	1559	TGFBP 4.
FT	DOMAIN	1606	1647	EGF-LIKE 27, CALCIUM-BINDING.
FT	DOMAIN	1648	1688	EGF-LIKE 28, CALCIUM-BINDING.
FT	DOMAIN	1689	1758	TGFBP 5.
FT	DOMAIN	1766	1807	EGF-LIKE 29, CALCIUM-BINDING.
FT	DOMAIN	1808	1848	EGF-LIKE 30, CALCIUM-BINDING.
FT	DOMAIN	1849	1890	EGF-LIKE 31, CALCIUM-BINDING.
FT	DOMAIN	1891	1929	EGF-LIKE 32, CALCIUM-BINDING.
FT	DOMAIN	1930	1972	EGF-LIKE 33, CALCIUM-BINDING.
FT	DOMAIN	1973	2012	EGF-LIKE 34, CALCIUM-BINDING.
FT	DOMAIN	2013	2054	EGF-LIKE 35, CALCIUM-BINDING.
FT	DOMAIN	2055	2121	TGFBP 6.
FT	DOMAIN	2122	2165	EGF-LIKE 36, CALCIUM-BINDING.
FT	DOMAIN	2166	2205	EGF-LIKE 37, CALCIUM-BINDING.
FT	DOMAIN	2206	2246	EGF-LIKE 38, CALCIUM-BINDING.
FT	DOMAIN	2247	2290	EGF-LIKE 39, CALCIUM-BINDING.
FT	DOMAIN	2291	2332	EGF-LIKE 40, CALCIUM-BINDING.
FT	DOMAIN	2333	2400	TGFBP 7.
FT	DOMAIN	2402	2443	EGF-LIKE 41, CALCIUM-BINDING.
FT	DOMAIN	2444	2484	EGF-LIKE 42, CALCIUM-BINDING.
FT	DOMAIN	2485	2523	EGF-LIKE 43, CALCIUM-BINDING.
FT	DOMAIN	2524	2566	EGF-LIKE 44, CALCIUM-BINDING.
FT	DOMAIN	2567	2606	EGF-LIKE 45, CALCIUM-BINDING.
FT	DOMAIN	2607	2647	EGF-LIKE 46, CALCIUM-BINDING.
FT	DOMAIN	2648	2687	EGF-LIKE 47, CALCIUM-BINDING.
FT	DISULFID	85	94	BY SIMILARITY.
FT	DISULFID	89	100	BY SIMILARITY.
FT	DISULFID	102	111	BY SIMILARITY.
FT	DISULFID	119	129	BY SIMILARITY.
FT	DISULFID	123	134	BY SIMILARITY.
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FT	DISULFID	150	160	BY SIMILARITY.
FT	DISULFID	154	166	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	250	262	BY SIMILARITY.
FT	DISULFID	257	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	304	BY SIMILARITY.
FT	DISULFID	299	313	BY SIMILARITY.
FT	DISULFID	315	328	BY SIMILARITY.
FT	DISULFID	453	465	BY SIMILARITY.
FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.

FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.
FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
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FT	DISULFID	617	628	BY SIMILARITY.
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FT	DISULFID	639	652	BY SIMILARITY.
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FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1285	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
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FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.
FT	DISULFID	1674	1687	BY SIMILARITY.

Query Match 11.5%; Score 172.5; DB 1; Length 2871;
Best Local Similarity 22.7%; Pred. No. 1.9e-05;
Matches 59; Conservative 17; Mismatches 81; Indels 103; Gaps 8;

Qy	26	PGRRCAVRAHAGDPVSESFVQVVPILTTCDGHR---ACSTYRTVTRATVRSGGLAPA	82
Db	75	PGGNOCIVPICRHSGGDFCSR---PNNCTPSSGDISPSCGS-RSIQHCHNRCNMGGSCS	130
Qy	83	RPRYACGPMWRRTSLPGACGAALICOPPCRNCGSCVQPGRCRCPAGWRGDTCO-----	135

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Db      . 131 DHCLGQKGYIGH-----CGQPVCESSGCLNGRCVAPNRCACVGTGFTGPQCDYRTGP 185
QY      136 -----S 136
Db      186 CFTVSNOMOGQGLSGIVCTKTLCCATVGRAMGHPCEMCPADPHPCRGFIPNIRTAGCQ 245
QY      137 DVDECSARRGCP-ORCINTAGSYWCQWEGHSLADGTL-----VPRGG--- 181
Db      246 DVDECOAIRPMCGGNCINTVGSFECCKPAHGKFNVSOKCEDIDECSTIPGVCDGGECT 305
QY      182 -----PPRVAPNPTG 191
Db      306 NTVSSYFCCKCPGFTSPDG 325

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Search completed: September 10, 2003, 17:13:31
 Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 17:10:27; Search time 19 seconds
(without alignments)
1381.792 Million cell updates/sec

Title: US-09-978-191a-506

Perfect score: 1505

Sequence: 1 MRGSOEVLIMLVLAVG3T.....SEQISFLEBOLGSCCKKDS 273

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435.5	28.9	293	2 T09065	hypothetical prote
2	256	17.0	1574	2 T13954	MEGF6 protein - ra
3	252.5	16.8	558	2 T13954	hypothetical prote
4	218	14.0	1620	2 T27283	hypothetical prote
5	196	13.0	1964	2 T09059	notch4 - mouse
6	189	12.6	678	2 B48089	growth arrest-spec
7	184	12.2	673	2 A48089	growth arrest-spec
8	183.5	12.2	2907	2 A57278	fibritillin-2 precu
9	180	12.0	810	2 T10756	Not-homolog protei
10	178	11.8	674	2 I55476	growth potentialin
11	176.5	11.7	3202	2 A47221	fibritillin-1 precu
12	175.5	11.7	2321	2 S78549	notch3 protein - h
13	174	11.6	835	2 J90076	notch3 protein - h
14	173.5	11.5	1247	2 NMHUND	notch3 protein - h
15	173	11.5	2703	2 A24200	notch3 protein - h
16	172.5	11.5	2871	2 A55624	notch3 protein - h
17	172	11.4	2531	2 A46019	notch3 protein - h
18	171.5	11.4	2871	2 A55567	notch3 protein - h
19	170	11.3	675	1 KXMS	plasma protein S p
20	170	11.3	2918	2 A54105	fibritillin-2 precu
21	169.5	11.3	2318	2 S45306	notch 3 protein -
22	169	11.2	833	2 S19087	gene Delta protein
23	168	11.2	675	1 KXRTS	plasma protein S p
24	166	11.0	832	2 A31246	neurogenic protein
25	166	11.0	880	2 S00670	neurogenic repetit
26	164	10.9	1429	2 S06434	homeotic protein 1
27	164	10.9	2524	2 A35844	Xotch protein - Af
28	164	10.9	3871	2 T22812	hypothetical prote
29	163.5	10.9	2555	2 A40043	notch protein homo

30	162	10.8	646	2 S38819	plasma protein S -
31	161	10.7	387	2 B49175	Notch A protein -
32	161	10.7	675	1 KXBOS	plasma protein S p
33	160.5	10.7	2531	2 S18188	notch protein homo
34	160	10.6	2437	2 S42612	transmembrane proc
35	158.5	10.5	407	1 KRB07	coagulation factor
36	158.5	10.5	456	1 KXBO	latent transforman
37	158	10.5	1820	2 A55494	plasma protein S p
38	157	10.4	676	1 KXHUS	plasma protein S p
39	156	10.4	1221	2 A49457	fibritillin-2 precu
40	156	10.4	1408	2 S16148	gene serrate prote
41	156	10.4	1408	2 KFHU7	coagulation factor
42	155.5	10.3	3635	2 T10053	laminin alpha 5 ch
43	155.5	10.3	2471	2 A49128	cell-fate determin
44	155	10.3	387	2 A49128	extracellular prot
45	154	10.2	387	2 A49128	extracellular prot

ALIGNMENTS

RESULT 1

T09065
hypothetical protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
C:Accession: T09065
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <ROM>
A:Cross-references: EMBL:AF030001; NID:G2564945; PID:G2564953
C:Genetics:
A:Map position: 17
A:Introns: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3; 280/1
C:Superfamily: unassigned EGF-related proteins; EGF homology
F:114-141/Domain: EGF homology <EGF>
F:148-183/Domain: EGF homology <EGF>

Query Match 28.9%; Score 435.5; DB 2; Length 293;
Best Local Similarity 37.3%; Pred. No. 8.9e-25;
Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;

QY	1	MRGSOEVLIMLVLAVG-GTE-HAYRGRVCARAHGDPV--SESFVGRVYOPFLTTC	56
DB	11	LRG-----LSFFVLMTGEGTRGGSFKESLGVCKOTLVLPLRYNESYQPVYKPYLTLC	65
QY	57	DGRACSTYRTTYTAYRSPGLAPARPRYACCPGKRTSGLPACGA-AICPPCRNGG	115
DB	66	AGRICSTYRTTYTAYRSPGLAPARPRYACCPGKRTSGLPACGA-AICPPCRNGG	122
QY	116	SCVPGRCRCAGRGKGTCSQDVDECSARGGCGQRCINTAGSWCCMEHSLSAGTL	175
DB	123	VCTPDRRCAPGCGKCHVDVDECRASLTLSHGCLNTLGSFLCSCHPLVLGLDGR	182
QY	176	CVPRGPRVAVNPFTGV-----DSAMKEEVORLQSRVDLLEKQLVLAPL	221
DB	183	CA--GPE--SPTASISLVANREADSEERLRLREVALRLRKLKQ-----	228
QY	222	HSLSQA--LEHGLP-DPSGLVHSGOQ--GRIDSLEQISFLEBOLGSCCKKDS	273
DB	229	--WATOGAWRAVLPMPELREPEQVAFELWGRGDRIESLSDVLLLERLGACACBDNS	286

RESULT 2

T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: GB:U13720; NID:9401766; PID:AAA58494.1; PID:9401767
F:41-92/Domain: Gla domain homology #status atypical <Gla>
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-297/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 12.6%; Score 189; DB 2; Length 678;
Best Local Similarity 34.2%; Pred. No. 2e-06;
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Qy 46 ORVOPFLITCDG-----RACSTYRTYTAARRSPGLAPARRVACC-----PGWK 93
Db 47 RRAQVFEBAKQGHLEBCEVBEIACS--REAREVEFENDEPDTDFYFPRYIDCINKYGSPT 104
Qy 94 RTSG-----LRGCGAALICPPC--RNGSGVOP--GR--CRCPAGRGDTCCSDVDEC 141
Db 105 KNSGATCVQNLDPDC---TPNCDRKQTQACQDLMGFCLCKAGWGRLCDKDVNCC 160
Qy 142 SARSGCFORCINTAGSYWCQCEGHSLSADTLIC 176
Db 161 SOENGGCLQICHNKRGSPHCCHSGFELSSDRTIC 195

RESULT 7
A48089
Growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
A:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: GB:X59846; NID:9407060; PID:CAA42507.1; PID:9407061
A:Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:38-89/Domain: Gla domain homology #status atypical <Gla>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 12.2%; Score 184; DB 2; Length 673;
Best Local Similarity 31.6%; Pred. No. 4.6e-06;
Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

Qy 46 ORVOPFLITCDG-----RACSTYRTYTAARRSPGLAPARRVACC----- 89
Db 44 RRAQVFEBAKQGHLEBCEVBEIACS--REAREVEFENDEPDTDFYFPRYIDCINKYGSPT 101
Qy 90 --PGW-KRTSGLPAC-----GAALCPPCRNKSGSCVOPGRCRCPAGMRGDTCCSDV 138

Db 102 KNDFEAKCVQNLDPDCTPNPCDKKCTHICQDLMG-----FECVCTDGMWGRLCDKDV 154
Qy 139 DECSARRGCGPCRCINTAGSYWCQCEGHSLSADTLIC 176
Db 155 NECVAKNGGCSQVCHNKRGSPHCCHSGFELSSDQTC 192

RESULT 8
A57278
Fibrillin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002
A:Accession: A57278
R:Zhang, H.; Hu, W.; Ramirez, F.
J. Cell. Biol. 129, 1165-1176, 1995
A:Title: Developmental expression of fibrillin gene suggests heterogeneity of extracell
A:Reference number: A57278; MUID:95263670; PMID:7744963
A:Accession: A57278
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-2907 <ZHA>
A:Cross-references: GB:U39790; NID:9762830; PID:AAA74908.1; PID:9762831
C:Superfamily: Fibrillin 1; EGF homology
F:1239-1274/Domain: EGF homology <EGF1>
F:2488-2523/Domain: EGF homology <EGF>

Query Match 12.2%; Score 183.5; DB 2; Length 2907;
Best Local Similarity 23.9%; Pred. No. 1.8e-05;
Matches 60; Conservative 19; Mismatches 85; Indels 87; Gaps 7;

Qy 2 RSGQVLLMWLLVLAVGTEHAY-----RGRRVCAVRAGDVSESFVQRYOPFLT 54
Db 77 RGQDEILNG-----PNCGRFRHSYCCPCPKMTLPBGNGQCLVPICRNCGGFGSR---PNNC 130
Qy 55 TCDGHRACST--YRTYTAARRSPGLAPARRVACCPCGKRTSGLPACGAALICQPPCR 112
Db 131 TCSSQGISPTGCRKSIQCCSVRCNMNGTCCADHCCQCGYIGT-----YCGQPVCENGCQ 185
Qy 113 NGSGVOPGRCRCPAGMRGDTCC-----SPVDECSARRGCGP--ORCINTAGSYWCQCE 165
Db 186 NGRGICGNRCACVYGVGFPGCEERDRTGPFCTQYNNMCGQGLTGICTKTLCCATIGR 245
Qy 136 -----SPVDECSARRGCGP--ORCINTAGSYWCQCE 165
Db 246 AMGHCCEMCPAPQPCRCRGLPNTRTGACQDVDECAALPGLCGGNCINTNGSFECRCRA 305
Qy 166 GHSLSADSTLC 176
Db 306 GHKQSETTQKC 316

RESULT 9
T10756
Nef-homolog protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
A:Accession: T10756
R:Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsushashi, S.; Kikkawa, U.
submitted to the EMBL Data Library, November 1998
A:Description: Protein kinase C-binding protein.
A:Reference number: Z17122
A:Accession: T10756
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <KUR>
A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180
A:Experimental source: strain Sprague-Dawley, brain

Query Match 12.0%; Score 180; DB 2; Length 810;
Best Local Similarity 36.5%; Pred. No. 1.1e-05;
Matches 35; Conservative 13; Mismatches 38; Indels 10; Gaps 3;

Qy 88 CCGWKRTSGLPACGAALICPPCRNKGSCVOPGRCRCPAGMRGDTCCSDVDECSARRGG 147

DB 504 CQPGVGN---GTCACACBECRCRGCVAPNKCVCSSGFTGSHCEKDIDECAGFVE 559

OY 148 CP--QRCINTAGSYWCQCBGH---SLSADGTLCV 177

DB 560 CHNYSRCVNLPGMYHCECRSGFHDDGTSLSGESCI 595

RESULT 10

15476

growth potentiating factor - rat

C:Species: Rattus sp. (rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001

A:Accession: 155476

R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.

J. Biol. Chem. 270, 5702-5705, 1995

A:Title: Vascular smooth muscle cell-derived, GLA-containing growth-potentiating factor

A:Reference number: 155476; PMID:95197586; PMID:7890695

A:Accession: 155476

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-674 <RES>

A:Cross-references: GB:D42148; NID:g1526567; PIDN:BA07719.1; PID:g983402

C:Superfamily: plasma protein S; EGF homology; GLA domain homology; laminin G repeat hom

F:29-89/Domain: GLA domain homology <GLA>

F:117-150/Domain: EGF homology <EG1>

F:157-192/Domain: EGF homology <EG2>

F:198-233/Domain: EGF homology <EG3>

F:239-274/Domain: EGF homology <EG4>

F:308-647/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 11.8%; Score 178; DB 2; Length 674;

Best Local Similarity 30.4%; Pred. No. 1,3e-05;

Matches 48; Conservative 8; Mismatches 66; Indels 36; Gaps 6;

OY 46 QRYVOPFLTCDGH-----RACSTYRTYTAARSPGLAPARPVAC----- 89

DB 44 RRAYVFEBAKQHLERECVEVCSEEA--KEVFENDEDTYFYRYGECRAKXGRPD 101

OY 90 --PGWKR-TSLGPAC-----GAITQPPCRNGSCVQPCRCPCPMRGDTQSDV 138

DB 102 KNPNFATVCVKNLPDQCTPNPCDKKQTQLQDLMGN-----FFCLCKDKGSGRLCDKDV 154

OY 139 DECSARRGGCPORCINTAGSYWCQCBGHSLSDGTLG 176

DB 155 NECSQKNGGSGVCHNKPSFQCACHSGPSLQSDNKC 192

RESULT 11

154721

fibrillin 1 precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C:Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R:Corson, G.M.; Chabery, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure

A:Reference number: A47221; PMID:94010947; PMID:7691719

A:Accession: A47221

A:Molecule type: mRNA

A:Residues: 1-337, 'T', 339-1029 <COR>

A:Cross-references: GB:X63556

R:Perle, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Panglman, T.; Bonad

Hum. Mol. Genet. 2, 961-968, 1993

A:Title: Genomic organization of the sequence coding for fibrillin, the defective gene F

A:Reference number: I54355; PMID:93372860; PMID:8364578

A:Accession: I54355

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 132-3002 <PER>

A:Cross-references: GB:U13923; PIDN:AA02036.1; PID:g306746

R:Masler, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.

Nature 352, 334-337, 1991

A:Title: Partial sequence of a candidate gene for the Marfan syndrome.

A:Reference number: S17064; PMID:91304568; PMID:1852207

A:Accession: S17064

A:Molecule type: mRNA

A:Residues: 1030-3002 <MAS>

A:Cross-references: EMBL:X63556

R:Dietz, H.C.; Valle, D.; Franccomano, C.A.; Kendzior, R.J.

Science 259, 680-683, 1993

A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.

A:Reference number: I59574; PMID:93157831; PMID:8430317

A:Accession: I59574

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 2217-2288, 'T', 2290-2325 <RES>

A:Cross-references: GB:S54426; NID:g264860; PIDN:AA025244.1; PID:g264861

R:Lee, B.; Godfrey, M.; Vitale, E.; Hoti, H.; Mattei, M.G.; Sarlati, M.; Tsipouras, P.

Nature 352, 330-334, 1991

A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe

A:Reference number: S17062; PMID:91304567; PMID:1852206

A:Accession: S17062

A:Molecule type: mRNA

A:Residues: 'VLTAVFILTSLYKML', 944-1444 <LEB1>

A:Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015

A:Accession: S62111

A:Molecule type: protein

A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEB2>

R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.

J. Biol. Chem. 264, 21381-21385, 1989

A:Title: Connective tissue microfibrils. Isolation and characterization of three large p

A:Reference number: A34198; PMID:90078246; PMID:2512293

A:Accession: A34198

A:Molecule type: protein

A:Residues: 565-575, 1890-1892, 'I', 1894-1900 <MAD>

C:Comment: Fibrillin is a major component of elastin-associated microfibrils.

C:Genetics:

A:Gene: GDB:FBNI

A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700

A:Map position: 15q21.1-15q21.1

A:Intons: 2236/1, 2258/1, 2297/1

C:Superfamily: Fibrillin 1; EGF homology

C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; f

F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted <MATC>

F:132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>

F:133-1367/Domain: EGF homology <EGF>

F:1457-1492/Domain: EGF homology <EGF2>

F:2262-2295/Domain: EGF homology <EGF1>

Query Match 11.7%; Score 176.5; DB 2; Length 3002;

Best Local Similarity 22.7%; Pred. No. 6e-05;

Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;

OY 26 PERRICAVRAHGDPISEFVQRYVOPFLTCDGH--ACSTYRTYTAARSPGLAPA 82

DB 206 PGNOCIPICRHSQGDPCSR---PNMCTPSSGIAPSCS-RSIQHCNIRCMNGSCS 261

OY 83 RERVACCPGWRKTSGLPACGAALQPCPRNGSCVQPCRCPCPMRGDTQSDV 135

DB 262 DDHCLCQKGYIGTH---CGPVCESGLANGRCVAPNRCACTYGTGPOCERDRTGP 316

OY 136 -----S 136

DB 317 CFTVSNMCGQLSGIVCTKQLCATVGRAMGRCMCPAQPHCRCRGFTPNRTGACQ 376

OY 137 DVDECSARRGGCP-ORCINTAGSYWCQCBGHSLSDGTLG-----VPRGG-- 181

DB 377 DVDECAIPGLCOGAGNCINTVGSFECPCPAHKLNEVSQKCEDIDECSTIPICBGECT 436

OY 182 -----PPRVAPNPTG 191

DB 437 NTVSSYFCKCPDGYTSPDG 456

RESULT 12

S78549

notch3 protein - human

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2002

C:Accession: S78549; S71825

R:Joutel, A.; Tournier-Lasserre, E.

submitted to the EMBL Data Library, April 1997

A:Reference number: S78549

A:Accession: S78549

A:Molecule type: mRNA

A:Residues: 1-2321 <J001>

A:Cross-references: EMBL:U97669; NID:G2668591; PIDN:AA91371.1; PID:G2668592

R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrialat, H.; Mouton, P.; Alamowicz, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.

Nature 383, 707-710, 1996

A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke

A:Reference number: S71825; MUID:97032728; PMID:8878478

A:Accession: S71825

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 67-113;138-194;268-333; 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <J002

A:Cross-references: EMBL:U97669

A:Genetics:

A:Gene: notch3

A:Map position: 19p13.1

C:Function:

A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

C:Keywords: tandem repeat; transmembrane protein

F:123-155/Domain: EGF homology <EGF1>

F:162-194/Domain: EGF homology <EGF1>

F:240-271/Domain: EGF homology <EGF2>

F:318-349/Domain: EGF homology <EGF3>

F:473-504/Domain: EGF homology <EGF4>

F:583-684/Domain: EGF homology <EGF5>

F:928-959/Domain: EGF homology <EGF6>

F:1838-1870/Domain: ankyrin repeat homology <AN1>

F:1871-1903/Domain: ankyrin repeat homology <AN2>

F:1905-1937/Domain: ankyrin repeat homology <AN3>

F:1938-1970/Domain: ankyrin repeat homology <AN4>

F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 11.7%; Score 175.5; DB 2; Length 2321;

Best Local Similarity 34.5%; Pred. No. 5.7e-05;

Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

Oy 56 CDGHRACSTYRTTYRATYRSPGLAPARPRVAC-CPGWRK--TSGLPAGCAAIQPPCR 112

Db 87 CAGRGVCS-----SVVAGTARFSCRCPRGRGPDGSLDPC-----LSPCA 129

Oy 113 NCGSC-VDP-GR--CRCPAGMRGDTCCQSDVDEC-----SARRGCGCRCLNTAGSWCCW 164

Db 130 HGARSVPDPDGFLLSCPPGYGRSCRSVDCECRVGEPCRHGG---TCINTPGSRCCCP 186

Oy 165 EGHSLADGTLCPKGGPPRVAHP 189

Db 187 AGYT---GFLCENPAVP--CAPSP 205

RESULT 13

JP0076

nel protein - chicken

C:Species: Gallus gallus (chicken)

C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 13-Aug-1999

C:Accession: A38963; JP0076

R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.

Dev. Dyn. 203, 212-222, 1995

A:Title: New gene, nel, encoding a Mr 93k protein with EGF-like repeats is strongly exp

A:Reference number: A38963; MUID:9583734; PMID:7655083

A:Accession: A38963

A:Molecule type: mRNA

A:Residues: 1-835 <MAT>

A:Cross-references: DDBJ:D45365

A:Experimental source: 9-day embryo

R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.

submitted to JIPID, January 1995

A:Description: A new gene, nel, encoding a Mr 93k protein with EGF-like repeats is stron

A:Reference number: JP0076

A:Accession: JP0076

A:Molecule type: mRNA

A:Residues: 1-835 <MA2>

A:Cross-references: DDBJ:D45365

A:Experimental source: 9-day embryo

C:Superfamily: von Willebrand factor type C repeat homology; EGF homology

F:273-333/Domain: von Willebrand factor type C repeat homology <WVC>

F:395-592/Region: EGF-like repeats

F:444-480/Domain: EGF homology <EGF1>

F:486-521/Domain: EGF homology <EGF2>

F:525-552/Domain: EGF homology <EGF3>

Query Match

Best Local Similarity 11.6%; Score 174; DB 2; Length 835;

Matches 30; Conservative 11; Mismatches 27; Indels 2; Gaps 1;

Oy 100 GACGAIQCPPCRNCGSCVQPERCRCPAGMRGDTCCQSDVDECARRGCGCPOR--CINTAG 157

Db 518 GTVCKAFCKDGRNGACIASNVCACPGFTGSPSCETIDECSDGFVQCDSRANCINLP 577

Oy 158 SYWCQMEGH 167

Db 578 WYHCRCRDGY 587

RESULT 14

MMHUND

nidogen precursor - human

N:Alternate names: entactin

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Oct-2000

C:Accession: A33322; A32437; A61367

R:Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlto

DNA 6, 581-594, 1989

A:Title: Human nidogen: complete amino acid sequence and structural domains deduced from

A:Reference number: A33322; MUID:90091745; PMID:2574658

A:Accession: A33322

A:Molecule type: mRNA

A:Residues: 1-1247 <NAG>

A:Cross-references: EMBL:M30269

R:Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.;

Am. J. Hum. Genet. 44, 876-885, 1989

A:Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to ch

A:Reference number: A32437; MUID:89270475; PMID:2471408

A:Accession: A32437

A:Molecule type: mRNA

A:Residues: 667-1247 <OLS>

A:Cross-references: EMBL:M27445; NID:G602466; PIDN:AAA57261.1; PID:G602467

A:Note: the authors translated the codon AAG for residue 966 as Cys

R:Fazio, M.J.; O'Leary, J.; Kaehner, V.M.; Chen, Y.Q.; Salter, B.; Vitro, J.

J. Invest. Dermatol. 97, 281-285, 1991

A:Title: Human nidogen gene: structural and functional characterization of the 5'-flanki

A:Reference number: A61367; MUID:91302882; PMID:1906509

A:Accession: A61367

A:Molecule type: DNA

A:Residues: 1-28 <PAZ>

C:Comment: This protein is a basement membrane glycoprotein that forms a complex with la

C:Genetics:

A:Gene: GDB:NID

A:Cross-references: GDB:120336; OMIM:131390

A:Map position: 19q31-q43

C:Superfamily: nidogen; EGF homology; LDL receptor YWTD-containing repeat homology; chr

C:Keywords: basement membrane; beta-hydroxyaspartagine; calcium binding; cell binding; co

protein

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-1247/Product: nidogen #status predicted <MAT>

F:390-425/Domain: EGF homology <EG1>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:13:38 ; Search time 21 Seconds

(without alignments)
267.752 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505
Sequence: 1 MRGSEVLLMMLVLAVAGT.....SEQISFLEQLGSCCKDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87302 seqs, 20596313 residues

Total number of hits satisfying chosen parameters: 87302

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1504	99.9	285	US-10-425-114A-37265	Sequence 37265, A
2	251.5	16.7	436	US-60-487-610-1532	Sequence 1532, A
3	251.5	16.7	553	US-60-487-610-1530	Sequence 1530, A
4	251.5	16.7	565	US-60-487-610-1531	Sequence 1531, A
5	223	14.8	509	US-09-908-576-315	Sequence 315, App
6	188.5	12.5	2003	US-60-487-610-1823	Sequence 1823, App
7	182	12.1	810	PCT-US02-29560A-361	Sequence 361, App
8	181	12.0	366	PCT-US03-25418-41	Sequence 41, App1
9	176.5	11.7	2871	US-60-490-890-481	Sequence 481, App
10	176.5	11.7	1587	US-60-487-610-1941	Sequence 1941, App
11	175.5	11.7	2321	US-60-487-610-2570	Sequence 2570, App
12	175.5	11.6	671	US-60-485-450-1335	Sequence 1335, App
13	173.5	11.5	1247	US-60-487-610-2260	Sequence 2260, App
14	173.5	11.2	604	PCT-US02-24483-4	Sequence 4, App1
15	168.5	10.9	1631	US-60-487-610-1861	Sequence 1861, App
16	163.5	10.9	2556	US-10-294-006-12	Sequence 12, App1
17	163.5	10.9	618	PCT-US02-29560A-301	Sequence 301, App
18	160.5	10.7	467	PCT-US02-24483-176	Sequence 176, App
19	158.5	10.5	1435	US-60-487-610-1817	Sequence 54, App1
20	158.5	10.5	1821	US-60-487-610-1817	Sequence 1817, App
21	158	10.5	1821	US-09-976-858-189	Sequence 1179, App
22	158	10.4	999	US-60-485-450-1179	Sequence 189, App
23	156	10.3	481	US-60-495-114-1951	Sequence 1951, App
24	155.5	10.3	481	US-60-495-114-1952	Sequence 1952, App
25	155.5	10.3	481	US-60-495-135-406	Sequence 406, App
26	155.5	10.3	481	US-60-495-135-406	Sequence 406, App

27	155.5	10.3	481	US-60-495-135-407	Sequence 407, App
28	155	10.3	630	PCT-US02-24483-2	Sequence 34, App1
29	154	10.2	874	US-10-294-006-34	Sequence 155, App
30	153	10.2	1218	US-10-648-593-155	Sequence 1228, App
31	151	10.0	524	PCT-US03-24084-2	Sequence 1228, App
32	151	10.0	1799	US-60-485-450-1228	Sequence 1228, App
33	151	10.0	1905	PCT-US02-05093-6	Sequence 6, App1
34	150	10.0	459	US-60-495-114-1953	Sequence 1953, App
35	150	10.0	459	US-60-495-114-1954	Sequence 1954, App
36	150	10.0	459	US-60-495-135-408	Sequence 408, App
37	150	10.0	459	US-60-495-135-409	Sequence 409, App
38	148	9.8	379	US-09-908-576-4	Sequence 4, App1
39	148	9.8	1185	US-60-485-450-1176	Sequence 1176, App
40	147	9.8	1184	PCT-US02-38594-6	Sequence 6, App1
41	146	9.7	2225	US-60-487-610-2532	Sequence 2532, App
42	145	9.6	986	US-60-487-610-2032	Sequence 2032, App
43	145	9.6	1132	US-60-487-610-2033	Sequence 2033, App
44	144.5	9.6	461	US-60-495-114-1137	Sequence 1137, App
45	144.5	9.6	461	US-60-495-135-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-10-425-114A-37265
Sequence 37265, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425, 114A
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37265
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB43-95-B8_F11.pep
US-10-425-114A-37265

Query Match 99.9%; Score 1504; DB 6; Length 285;
Best Local Similarity 99.6%; Pred. No. 1.7e-108;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMMLVLAVAGTTHAYRPGRRVCAVAHAGDPVSESPVORYOPLTTCDGHR 60
DB 13 MRGSEVLLMMLVLAVAGTTHAYRPGRRVCAVAHAGDPVSESPVORYOPLTTCDGHR 72
QY 61 ACSTYRTYRTRAYRRSPGLAPARPRVACCPMKRTSGIPGCGAICOPPRNGSCVOP 120
DB 73 ACSTYRTYRTRAYRRSPGLAPARPRVACCPMKRTSGIPGCGAICOPPRNGSCVOP 132
QY 121 GRCCPAGMRDTCOSPDVDECSARGGCPCCITAGSYMCQCEGHSLSADGTLCPKG 180
DB 133 GRCCPAGMRDTCOSPDVDECSARGGCPCCITAGSYMCQCEGHSLSADGTLCPKG 192
QY 181 GPPVAPNPTGVDSAMKEEVORLQSRVLDLEKQLVLAFLHSLASQALEHGLDPDPSLL 240
DB 193 GPPVAPNPTGVDSAMKEEVORLQSRVLDLEKQLVLAFLHSLASQALEHGLDPDPSLL 252
QY 241 VHSFOQGRIDLSLEQISFLEQLGSCCKKDS 273
DB 253 VHSFOQGRIDLSLEQISFLEQLGSCCKKDS 285

```

RESULT 2
US-60-487-610-1532
; Sequence 1532, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1532
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1532

```

PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 315
LENGTH: 509
TYPE: PRT
ORGANISM: Homo Sapien
US-09-908-576-315

Query Match 14.8%; Score 223; DB 5; Length 509;
Best Local Similarity 42.4%; Pred. No. 5,4e-10;

Matches 42; Conservative 13; Mismatches 40; Indels 4; Gaps 3;

QY 76 SEGLAPAPRYACPCGKRTSGLPAGCAAIQPPCRNGSCVOPGRCPAGMRGDTQ 135
DB 32 SIGLCRYGRIRICCGMAROSW--GQC-QPVCPGRCKH-GEICGNKCKCHGVAKTGN 87

QY 136 SDVECSARRGCCPQPCINTAGSYWCQCEHSLSADGT 174
DB 88 QDLNECGHLPKPCRKCMATYGSYKCYCINGYMLMDGS 126

RESULT 6
US-60-487-610-1823
Sequence 1823, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 2003
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-1823

Query Match 12.5%; Score 188.5; DB 7; Length 2003;
Best Local Similarity 29.6%; Pred. No. 1.1e-06;

Matches 61; Conservative 17; Mismatches 87; Indels 41; Gaps 11;

QY 80 APAPRYACPCGK-RTISGLPAGCAAIQPPCRNGSCVOPG--RCRCPAGMRGDTQ 135
DB 137 ASGRPOCSGCMGTGECQDLDFCSA---NPCVNGVCLATYPOIQCHCPGFEHFACE 192
QY 136 SDVECSARRGCCPQ-RCINTAGSYWCQCEHSLSADGTICVYKGG--PPRYAPNPTG 191
DB 193 RDVNECFDPPGCPGCTGSHNTLSFQCLCPVQ---EGPRCEIRAPCPRGCSN--GG 247
QY 192 VDSAMKEEVORLQSRVLLLEKTLQVLAPLHSLASQALEHGLPD---PGSLVHSPQOL 247

DB 248 TCOLMPEK-----DSTFHLCLCPFGI-----PDCEVNPDMCVSHQCGNG 288
QY 248 GRI-DLSLEQISFLEQJGSCCKXD 272
DB 289 GTCCGDLDTYTCLCPETWTGWDCESD 314

RESULT 7
PCT-US02-29560A-361
Sequence 361, Application PC/TUS0229560A
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnick, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 361
LENGTH: 810
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29560A-361

Query Match 12.1%; Score 182; DB 1; Length 810;
Best Local Similarity 37.5%; Pred. No. 1.3e-06;

Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 88 CTPGKRTSGLPAGCAAIQPPCRNGSCVOPGRCPAGMRGDTQSDVDECSARRGG 147
DB 504 CKPFGVGN---GTCRPFCEGCRYGTCVAPNKCVPSPGFTSHCEKIDCESEGLE 559
QY 148 C--PQPCINTAGSYWCQCEHSLSADGTICV 177
DB 560 CHNHRVCVNLPGWYHCEGRSGFDDGTYSLSGESCI 595

RESULT 8
PCT-US03-25418-41
Sequence 41, Application PC/TUS0325418
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION
APPLICANT: ELIOTT, Vicki S.
APPLICANT: KHARE, Reena
APPLICANT: EMERLING, Brooke M.
APPLICANT: KABLE, Amy E.
APPLICANT: TRAN, Uyen K.
APPLICANT: JIN, Pei
APPLICANT: BECHA, Shanya D.
APPLICANT: MARQUIS, Joseph P.
APPLICANT: SWARNAKAR, Anita
APPLICANT: SHAWLA, Narinder K.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: HAFALIA, April J.A.
APPLICANT: LEE, Soo Yeun
APPLICANT: JIANG, Xin
APPLICANT: JACKSON, Alan A.
APPLICANT: RICHARDSON, Thomas W.
APPLICANT: BLAKE, Julie J.
APPLICANT: WANG, Jonathan T.
APPLICANT: CHIEN, David
APPLICANT: YANG, Yonghong G.

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; TITLE OF INVENTION: CELL ADHESION AND EXTRACELLULAR MATRIX PROTEINS
; FILE REFERENCE: PF-1500 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25418
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: US 60/403,781
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 60/407,034
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/410,566
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/413,482
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,890
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/424,904
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/426,222
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7522915CD1
PCT-US03-25418-41

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Query Match      12.0%; Score 181; DB 1; Length 366;
Best Local Similarity 27.6%; Pred. No. 6.1e-07;
Matches 67; Conservative 23; Mismatches 65; Indels 88; Gaps 14;

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QY 12 LVLVAVGGR-----EHAYRRGRVCAVRAGDPVSEFVQRVQPF-----LTTCDGHA 61
DB 24 LLLALAGHTWYREBPQDGDREIC-----SESKIAITTKYPCCLKSSGELTTC----- 69
QY 62 CSTYRTIVAYRSPGLAPAPRPVYACCPGWMKRTSG--LP---GACGAATCOPPCNGGS 116
DB 70 -----YRKK-----CCKGYKRVLGQCIPEDYDVCAEAPCQOQCTDNG 107
QY 117 CYPGRCRCPAGWRCGT-----CQSDVDECSARRGG--CPORCINTAGSYWCQWE 165
DB 108 RV---LCTCYPGRYRERHRRKREKPYC--LDIDECASNGTLCAHICINTLGSYCECRE 163
QY 166 GHSLSADGTLVCKGPPRVAPNPVTGVSDA-----MKERVQLQSV 207
DB 164 GYRREDGKTCY-RGDK---YFNDTGHSEKSNVYAGTCCATCKEFYQMKQTVLQKXI 219
QY 208 DIL 210
DB 220 ALL 222

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RESULT 9
PCT-US03-25418-3
; Sequence 3, Application PC/TUS0325418
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: ELLIOTT VICKI S.
; APPLICANT: KHARE, Reena
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: KABLE, Amy E.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: JIN, Pei
; APPLICANT: BECHA, Shanya D.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: CHAWLA, Nandinder K.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: JIANG, Xin

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; APPLICANT: JACKSON, Alan A.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: BLAKE, Julie J.
; APPLICANT: WANG, Jonathan T.
; APPLICANT: CHIEN, David
; APPLICANT: YANG, Yonhong G.
; TITLE OF INVENTION: CELL ADHESION AND EXTRACELLULAR MATRIX PROTEINS
; FILE REFERENCE: PF-1500 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25418
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: US 60/403,781
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 60/407,034
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/410,566
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/413,482
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,890
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/424,904
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/426,222
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7513607CD1
PCT-US03-25418-3

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Query Match      11.7%; Score 176.5; DB 1; Length 393;
Best Local Similarity 27.4%; Pred. No. 1.5e-06;
Matches 55; Conservative 16; Mismatches 65; Indels 65; Gaps 8;

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QY 54 TTCGHRACSTYRTIVAYRSPGLAPAPRPVYACCPGWMKRTSGLPACGAATC-QPPC 111
DB 86 TPADGRKRGSKYLVADHEVHTCNPFRLVGPSSVYCLPNTGTGEPHCRGISSECSQPC 145
QY 112 RNGSGCYO-----PGR-----C 123
DB 146 QNGGTCVGVNVQYRCICPFGTGNRCQHQQTAAPEGSVAGDSAFSAPRCAQYERAOHC 205
QY 124 RCPAGWR-----GPTCOSDVDECSARRGGCPQ--RCINTAGSYWC---QCWEGHSLADG 173
DB 206 SCEAGFHLGSAAGDSVQCDVDECVGLQPVCPQGTTCINTGSGFQVSGPECEG-----SG 260
QY 174 TLCVPKGGPPRVAPNPVTGVS 194
DB 261 NVSYVKTSPFQGERNPCEMDS 281

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```

RESULT 10
US-60-490-890-481
; Sequence 481, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: LI, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: JACKSON, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 481
; LENGTH: 2871

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TYPE: PRT
ORGANISM: Homo sapiens
US-60-490-890-481

Query Match 11.7%; Score 176.5; DB 7; Length 2871;
Best Local Similarity 22.7%; Pred. No. 1.4e-05;
Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;

QY 26 PGRVCAVRAHGDVSESVFVORVYOPFLTTCDGHR---ACSTYRTTYRTAVRSPGLAPA 82
DB 75 PGNACTIPICHSGDGFCSR---PNMCTCPSGQAPBCGS-RSQHGNITCMANGSGS 130
QY 83 RPRVACBPWKRTSGLPAGCAIQCPCRNAGSCVOPRCRCPPAGWRGDTQC----- 135
DB 131 DDHCCQCGYIGTH-----CGQPVCESGCLNGRCVAPNRCACTGTGTGCCERDVRTGP 185
QY 136 -----S 136
DB 186 CFTVSNOWCQGLSGIVCTKTLCAATVGRAMGHPCEMCPAOPHPORRGFIPIRTGAQ 245
QY 137 DVDECSARRGGCP-ORCINTAGSYWCQCEGHSLSADGTLG-----VPRKG--- 181
DB 246 DVDECOALPGLCQCGNCINTVGSFECKCPAGHKLVESQKCEDIDECSTTIPGICGGECT 305
QY 182 -----PPRVAHPNPTG 191
DB 306 NTVSSYFCCKCPRGFTTSPDG 325

RESULT 11
US-60-487-610-1941
Sequence 1941, Application US/60487610

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1941
LENGTH: 1587
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-1941

Query Match 11.7%; Score 176; DB 7; Length 1587;
Best Local Similarity 39.8%; Pred. No. 7.9e-06;
Matches 39; Conservative 6; Mismatches 41; Indels 12; Gaps 3;

QY 82 ARPRVACBPWKRTSGLPAGCAIQCPCRNAGSCVOPG--RCRCPAGWRGDTQSDVD 139
DB 625 AAPHAGSCQDVDECTOSPELGGRAKXN-----LPGSFRVCVCPAGFRSACEEDVD 675
QY 140 ECSARRGGC-PORCINTAGSYWCQCEGHSLSADGTLG 176
DB 676 ECAOEPPECGRCDNTAGSFHACAPAGFRSRGAPC 713

RESULT 12
US-60-487-610-2570
Sequence 2570, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610

CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2570
LENGTH: 2321
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2570

Query Match 11.7%; Score 175.5; DB 7; Length 2321;
Best Local Similarity 34.5%; Pred. No. 1.3e-05;
Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY 56 CDGHRACSTYRTTYRTAVRSPGLAPARRYAC-CPGWR--TSGLPAGCAIQCPCR 112
DB 87 CAGRGVCS-----SVAGTARFSRCRCRFRFGDCLPDPCC-----LSPTCA 129
QY 113 NGGSC-VOP-GR--CRCPAGWRGDTQSDVDEC---SARRGGCPORCINTAGSYWCQW 164
DB 130 HGARCSVGPDRFLCSPPGYQGRSCRSDVDCECRVGEPCRHGG---TCLNTPGSPRCOP 186
QY 165 EGHSLADGTLCPKGPAPRVAHP 189
DB 187 AGYT---GPLCENPAVP--CAPSP 205

RESULT 13
US-60-485-450-1335
Sequence 1335, Application US/60485450

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
FILE REFERENCE: CLO01470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1335
LENGTH: 671
TYPE: PRT
ORGANISM: Homo sapiens
US-60-485-450-1335

Query Match 11.6%; Score 175; DB 7; Length 671;
Best Local Similarity 33.1%; Pred. No. 3.5e-06;
Matches 60; Conservative 10; Mismatches 57; Indels 54; Gaps 13;

QY 25 RPRRV-----CAVRAHGDVSESVFVORVYOPFLTTCDGHRACSTYRTTYRTAVRSPG 78
DB 307 RPFGLDLDTLVTCASR---NCCSS-----PCRGATCV----- 337
QY 79 LAPARRYAC-CP-GWKRTSGLPAGCAIQCPCRNAGSCVOPG--RCRCPAGWR-- 130
DB 338 LCPHKNYTCRCPPQYQDLSQDLCDVDVDECQDSFCAQ--ECVNTPGFRCECWGVYEPG 395
QY 131 --GDTQSDVDECSARRGGCPORCINTAGSYWCQCEGHSLSA-DGTL-----CVPRKG 181
DB 396 GPGEGACQDVDECALGRSPCAQCGCNTTDSFHCSCBEGYVLAGEBGTQCDVDCEVGG 455
QY 182 P 182
DB 456 P 456

RESULT 14
US-60-487-610-2260
Sequence 2260, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele

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; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; NUMBER OF SEQ. ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 2260
; LENGTH: 1247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2260

Query Match      11.5%; Score 173.5; DB 7; Length 1247;
Best Local Similarity 25.8%; Pred. No. 9.3e-06;
Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;

QY 20 TEHAYRPRRV-----CAVRAHG-----DPVSEFVGRVYQPFLLTCDGHRACSTYR 66
DB 681 TNACAPRPTQTCTECSTGFRDGRCTYDIDECSE-----QP---SVCGSHTTGNH- 730
QY 67 TIYTRAYRSPGLAPRPRYACCPGKMTSGLPAGACGALCOPP-----CRNG----- 114
DB 731 -----PGTFRCCEVGEYQFSD--EGTCVAVVDQGRPIVYCETGLHNCIDIPQR 774
QY 115 GSCVQG-----RCRCAGMRGD--TQSDVDECSARGGCPORCINTAGSYWCQCEGHS 168
DB 775 AQCITYGGSSYTCCLPGFSGDQACQ-DVDECQPCRCHDAPFCYNTPGSFQCKRQY- 832
QY 169 LSADGTLVCP-----KCGPRVAPNPTG----- 191
DB 833 -QGDGRFCVPGVEKRCQHERHILGAAGATDPQPIPPGLFVPCDAGHAPQCGH 891
QY 192 -----VDSAMKEVQRLQSRVLLLEKIQVLAPLH-SLSQALEHGLPDPGSLVHS 243
DB 892 STGYCWCVDPRDGR-EVEGRTRPGRMTPPCISTVAPPIHQPAPVAVIPLP-PGTHLL-- 947
QY 244 PQQLGRIDSL 253
DB 948 PAOTKIERL 957

RESULT 15
PCT-US02-24483-4
; Sequence 4, Application PC/TUS0224483
; GENERAL INFORMATION:
; APPLICANT: Curagen Corp. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416A-061
; CURRENT APPLICATION NUMBER: PCT/US02/24483
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ. ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ. ID NO 4
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-24483-4

Query Match      11.2%; Score 168.5; DB 1; Length 604;
Best Local Similarity 24.1%; Pred. No. 9.8e-06;
Matches 60; Conservative 16; Mismatches 78; Indels 95; Gaps 9;

QY 74 RRSPLAPARR-----YACCPGKMTSGLPAGACGALCOPPCRNNGSCVQPG 121
DB 27 RRPFGHFAERRRILGPHVCLSGFGSCCPGMAPSMG--GGHCTLLPLCSFGC--GSGICIAFN 84
QY 122 RCRCPAGMRGDTQ-----SDVD 139
DB 85 VSCQDQDEGATCPETHGRCGEYGCDDLCSHGCOEVARVCPVGRSMETAVGIRCTDID 144
QY 140 ECSARRGCPORCINTAGSYWCQCEGHSLSAD-----GTLCPK----- 179
DB 145 ECVT--SSCEGHCVTGEGFVCECGPGWQLSADHSCQDTDECLGTPOCQRCXNSIGSYX 202
QY 180 -----GAPPRVAPNPTGV--DSAMKEVQRLQSRVLLLEKIQVLAPLHSLASQ 227
DB 203 CSCTGFLHGNRRHSCVAFPAVALAPSATLDPORHPSKMLLLPBPAGPALSPGHSPPS- 261
QY 228 ALEHGLPDP 236
DB 262 ----GAPGP 266

Search completed: September 10, 2003, 17:23:33
Job time : 22 secs

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Db 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEHSLSDAGTLCVPGK 180
Qy 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSL 240
Db 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSL 240
Qy 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKKDS 273

RESULT 4
US-09-298-531-2
; Sequence 2, Application US/09298531
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T125-RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/074001
; CURRENT APPLICATION NUMBER: US/09/298,531
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: US 09/065,363
; EARLIER FILING DATE: 1998-04-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-531-2

Query Match 100.0%; Score 1505; DB 16; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSQEVLLMLLVLAAGTEHAYRPGRRVCAVRAHGDVSSFPQRYVQPELTTCGHR 60
Db 1 MRSQEVLLMLLVLAAGTEHAYRPGRRVCAVRAHGDVSSFPQRYVQPELTTCGHR 60
Qy 61 ACSTRTTYRTAYRSPGLAPRPAVACCPGKRTSGLPAGAGALICPPCNGGSCVOP 120
Db 61 ACSTRTTYRTAYRSPGLAPRPAVACCPGKRTSGLPAGAGALICPPCNGGSCVOP 120
Qy 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEHSLSDAGTLCVPGK 180
Db 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEHSLSDAGTLCVPGK 180
Qy 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSL 240
Db 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSL 240
Qy 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKKDS 273

RESULT 5
US-09-380-138-506
; Sequence 506, Application US/09380138
; GENERAL INFORMATION:
; APPLICANT: Wood, William I.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Yuan, Jean
; APPLICANT: Baker, Kevin P.
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2630RIE
; CURRENT APPLICATION NUMBER: US/09/380,138
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: US 60/077,450
; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: US 60/077,632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,791
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; PRIOR APPLICATION NUMBER: US 60/080,105
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; PRIOR APPLICATION NUMBER: US 60/081,071
; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: US 60/081,952
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR APPLICATION NUMBER: US 60/084,366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: US 60/084,441
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; PRIOR APPLICATION NUMBER: US 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 60/085,704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/086,023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/086,486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/087,208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,038
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 538
; SEQ ID NO 506
; LENGTH: 273
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-380-138-506

Query Match 100.0%; Score 1505; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLVLAVGCTGTHAIPGRVAVRAHGDVSESVQRYVQPLTTCDGR 60
DB 1 MRGSEVLLMLVLAVGCTGTHAIPGRVAVRAHGDVSESVQRYVQPLTTCDGR 60
QY 61 ACSTRTTYRTAYRRSPGLAPRPVACCPMKRTSGLPACGAICOPPRNGSSCVOP 120
DB 61 ACSTRTTYRTAYRRSPGLAPRPVACCPMKRTSGLPACGAICOPPRNGSSCVOP 120
QY 121 GRCRCPAGWRDTCQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLADGTLVCPKG 180
DB 121 GRCRCPAGWRDTCQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLADGTLVCPKG 180
QY 181 GPRPAPPTGVDSAMKEEVORLQSRVDLLEKQLVLAFLHSLASQALEHGLDPGSL 240
DB 181 GPRPAPPTGVDSAMKEEVORLQSRVDLLEKQLVLAFLHSLASQALEHGLDPGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEEOIGSCSKCKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEEOIGSCSKCKDS 273

RESULT 6
US-09-380-138-508
; Sequence 508, Application US/09380138
; GENERAL INFORMATION:
; APPLICANT: Wood, William I.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Yuan, Jean
; APPLICANT: Baker, Kevin P.
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2630RIE
; CURRENT APPLICATION NUMBER: US/09/380,138
; CURRENT FILING DATE: 1999-08-25
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[illegible]

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; PRIOR APPLICATION NUMBER: US 60/085,580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/086,023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/086,486
; PRIOR FILING DATE: 1998-05-22
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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,430
; PRIOR FILING DATE: 1998-05-22
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,038
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 538
; SEQ ID NO 508
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-138-508

Query Match      100.0%; Score 1505; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSQSEVLLMLLVLAAGCTEHAHYPGRVCAVRAHGDVSESFVQRYOPLTTCDHR 60
DB      1 MRSQSEVLLMLLVLAAGCTEHAHYPGRVCAVRAHGDVSESFVQRYOPLTTCDHR 60

QY      61 ACSTYRTITRYAHRSPGLAPAPRYAACCPGWKRTSGLPAGCGAALICPPCRNGSCVQ 120
DB      61 ACSTYRTITRYAHRSPGLAPAPRYAACCPGWKRTSGLPAGCGAALICPPCRNGSCVQ 120

QY      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180
DB      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180

QY      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180
DB      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180

QY      181 GPPRAVNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
DB      181 GPPRAVNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY      241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273
DB      241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273

RESULT 7
US-09-790-264-10
; Sequence 10, Application US/09790264
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodheart, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
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; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-790-264-10

Query Match      100.0%; Score 1505; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSQSEVLLMLLVLAAGCTEHAHYPGRVCAVRAHGDVSESFVQRYOPLTTCDHR 60
DB      1 MRSQSEVLLMLLVLAAGCTEHAHYPGRVCAVRAHGDVSESFVQRYOPLTTCDHR 60

QY      61 ACSTYRTITRYAHRSPGLAPAPRYAACCPGWKRTSGLPAGCGAALICPPCRNGSCVQ 120
DB      61 ACSTYRTITRYAHRSPGLAPAPRYAACCPGWKRTSGLPAGCGAALICPPCRNGSCVQ 120

QY      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180
DB      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180

QY      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180
DB      121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTL 180

QY      181 GPPRAVNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
DB      181 GPPRAVNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY      241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273
DB      241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273

RESULT 8
US-09-918-585A-506
; Sequence 506, Application US/0918585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
```

APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630p1c1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/086023
/ PRIOR FILING DATE: 1998-05-18
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Query Match      100.0%  Score 1505; DB 24; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 MGGSEVLLMLVLA VGGTEHAYRGRVCAVRAHGDVSSSFVQVYQPLTTCDDR 60
QY      61 AASTRTTIRTA YRSPGLAPARPRYACCPGKRTISGLPGACGAACOPPCRNSSCVOP 120
DB      61 AASTRTTIRTA YRSPGLAPARPRYACCPGKRTISGLPGACGAACOPPCRNSSCVOP 120
QY      121 GRCRCFAGMRGDTCCSDVDECSARRGCCPQRCINTAGSYWCOCWEGHSLADGTLCPK 180
DB      121 GRCRCFAGMRGDTCCSDVDECSARRGCCPQRCINTAGSYWCOCWEGHSLADGTLCPK 180
QY      121 GRCRCFAGMRGDTCCSDVDECSARRGCCPQRCINTAGSYWCOCWEGHSLADGTLCPK 180
DB      121 GRCRCFAGMRGDTCCSDVDECSARRGCCPQRCINTAGSYWCOCWEGHSLADGTLCPK 180
QY      181 GPPRAVNPVTGVDASAMKEEVQRIQSRVDLLEKTLQVLA PLHSLSQALEHGLPPGSL 240
DB      181 GPPRAVNPVTGVDASAMKEEVQRIQSRVDLLEKTLQVLA PLHSLSQALEHGLPPGSL 240
QY      241 VHSFOOLGRIDSLSBOISFLEROLGSCGCKXS 273
DB      241 VHSFOOLGRIDSLSBOISFLEROLGSCGCKXS 273

RESULT 9
US-09-918-585A-508
; Sequence 508, Application US/09918585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
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/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C1
/ CURRENT APPLICATION NUMBER: US/09/918,585A
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
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/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
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/ PRIOR APPLICATION NUMBER: 60/080105
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18

Query Match 100.0%; Score 1505; DB 24; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLVLAVGCTEHAYRPGRRVCAVRAHGDVSESFVQRYVQPFLLTTCGHR 60
DB 1 MRGSEVLLMLVLAVGCTEHAYRPGRRVCAVRAHGDVSESFVQRYVQPFLLTTCGHR 60
QY 61 ACSTRTTYRTAYRSPGLAPRPYACCPGKXTSGLPGAGAIQCPPRNGSCVOP 120
DB 61 ACSTRTTYRTAYRSPGLAPRPYACCPGKXTSGLPGAGAIQCPPRNGSCVOP 120
QY 121 GRCCPAGMRDTCOSDVDECSARGGCPQRCINTAGSYWCQMEGHSLSADGTLCPYKG 180
DB 121 GRCCPAGMRDTCOSDVDECSARGGCPQRCINTAGSYWCQMEGHSLSADGTLCPYKG 180
QY 181 GPPVAPNPTGVDSAMKEEVORLOSRYDLLEKQLVLIAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPVAPNPTGVDSAMKEEVORLOSRYDLLEKQLVLIAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRISLSQOTSFLEOLGSCSCCKDS 273
DB 241 VHSFOQLGRISLSQOTSFLEOLGSCSCCKDS 273

RESULT 10

US-09-978-187B-506
; Sequence 506 Application US/09978187B
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavitt, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C5
; CURRENT APPLICATION NUMBER: US/09/978,187B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,66-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLVLAVGSTEHAHYRGRVCAVRAHGPVSESFYQRYVQPELTTCDDHR 60
DB 1 MRGSEVLLMLVLAVGSTEHAHYRGRVCAVRAHGPVSESFYQRYVQPELTTCDDHR 60
QY 61 ACSTRTTYRTYRSPGLAPRPYACCPGKRTSGLPACGAACOPPCNNGSCVQOP 120
DB 61 ACSTRTTYRTYRSPGLAPRPYACCPGKRTSGLPACGAACOPPCNNGSCVQOP 120
QY 121 GRCRCPAMRGDTCCSDVDECGARRGGCPCRCINTAGSYWCOCWGHSHSADGTLCPVKG 180
DB 121 GRCRCPAMRGDTCCSDVDECGARRGGCPCRCINTAGSYWCOCWGHSHSADGTLCPVKG 180
QY 181 GPPRVAHPNTGVDSAMKEEVQRLQSRVLDLEBKQLVLAPLHSLASQALEHGLPDGSL 240

DB 181 GPPRVAHPNTGVDSAMKEEVQRLQSRVLDLEBKQLVLAPLHSLASQALEHGLPDGSL 240
QY 241 VHSFOOLGRIDSLSROISFLEOLSCSCCKOS 273
DB 241 VHSFOOLGRIDSLSROISFLEOLSCSCCKOS 273

RESULT 11
US-09-978-187B-508

Sequence 508, Application US/09978187B
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
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APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PICS
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27

PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MRGSEVLLMWLLVLAAGTEHAYRGRRCVCAVRAHDDPVSESVQRYVQPFLLTCGHR 60
Db 1 MRGSEVLLMWLLVLAAGTEHAYRGRRCVCAVRAHDDPVSESVQRYVQPFLLTCGHR 60

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QY 61 ACSTYRTITRTATRRSPGIALPAPRRYACCPGWRKRTSGLPACCAAIICPPCRNGSSCVOP 120
DB 61 ACSTYRTITRTATRRSPGIALPAPRRYACCPGWRKRTSGLPACCAAIICPPCRNGSSCVOP 120
QY 121 GRCRCAGMRGDTCCOSDVBCSARRGGCCORCNTNGSWCCWCEHSHLSAGTLCVPFG 180
DB 121 GRCRCAGMRGDTCCOSDVBCSARRGGCCORCNTNGSWCCWCEHSHLSAGTLCVPFG 180
QY 181 GPPRVAPNPTGVDSNAKKEVQRLOSRVDLLEKLOVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRVAPNPTGVDSNAKKEVQRLOSRVDLLEKLOVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLBEOGSCSCCKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLBEOGSCSCCKDS 273

RESULT 12
US-09-978-188A-506
/ Sequence 506, Application US/09978188A
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Pan, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC8
/ CURRENT FILING DATE: US/09/978,188A
/ PRIOR APPLICATION NUMBER: 2001-10-15
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077641
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
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/ PRIOR APPLICATION NUMBER: 60/079728
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/ PRIOR APPLICATION NUMBER: 60/082568
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082569
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082704
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082804
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085579
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGGSEVLLMLVLAAGCTEHAIRPGRVCAVAHAGPVSESVYQRYQFFLTTCGHR 60
Db 1 MGGSEVLLMLVLAAGCTEHAIRPGRVCAVAHAGPVSESVYQRYQFFLTTCGHR 60
Qy 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGKERTSGIPGACGAACOPPRNGSCVQP 120
Db 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGKERTSGIPGACGAACOPPRNGSCVQP 120
Qy 121 GRCPCAGMRGDTQCSVDYDECSARBGCPQRCINTAGSYWCQCWGHSLADGTLCPVK 180
Db 121 GRCPCAGMRGDTQCSVDYDECSARBGCPQRCINTAGSYWCQCWGHSLADGTLCPVK 180
Qy 181 GPRVAPPTGVDSAMKEVORLQSRVDLAEKQLVYLAPLHSLASQALHEGLDPPSLL 240
Db 181 GPRVAPPTGVDSAMKEVORLQSRVDLAEKQLVYLAPLHSLASQALHEGLDPPSLL 240
Qy 241 VHSFOQLGRIDSLSEQISFLEBOLGSCSKKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLEBOLGSCSKKDS 273

RESULT 13
US-09-978-188A-508
Sequence 508, Application US/09978188A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C8
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450

[illegible]

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGEVLMLVLAAGTEHAYRPRRCVCAVAHDDPSESVQAVYQVYPTLTDGHR 60
DB 1 MRSGEVLMLVLAAGTEHAYRPRRCVCAVAHDDPSESVQAVYQVYPTLTDGHR 60
QY 61 ACSTYRTTYTAVRSPGLAPAPRYVACCPGMRKTSGLPGACGALCQPCRNAGSCVOP 120
DB 61 ACSTYRTTYTAVRSPGLAPAPRYVACCPGMRKTSGLPGACGALCQPCRNAGSCVOP 120
QY 121 GRCRCPAGMRDTCQSDVDECSARGGCPCRCINTAGSYWCQCEGHSLSADGTLCPKG 180
DB 121 GRCRCPAGMRDTCQSDVDECSARGGCPCRCINTAGSYWCQCEGHSLSADGTLCPKG 180
QY 181 GPPRVAPNPTGVSAKKEEVORLOSRVLLLEKLOVLAPLHLSAQLAHLGPPDGSL 240
DB 181 GPPRVAPNPTGVSAKKEEVORLOSRVLLLEKLOVLAPLHLSAQLAHLGPPDGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEQOLGSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEQOLGSCCKKDS 273

RESULT 14
US-09-978-189-506
Sequence 506, Application US/09978189
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
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PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/080334
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/081071
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229

;; PRIOR FILING DATE: 1998-04-09
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;; PRIOR APPLICATION NUMBER: 60/082569
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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
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;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLVAVGTEHAYRPGRRVCAVBAHGDVSESSFVQRYQPFLLTTCGHR 60
DB 1 MRGSEVLLMWLVAVGTEHAYRPGRRVCAVBAHGDVSESSFVQRYQPFLLTTCGHR 60
QY 61 ACSTYRTTYRTAARSPCLAPARPRVACCPGMRKRTSGLPACGAAICQPPRNGSCVQ 120
DB 61 ACSTYRTTYRTAARSPCLAPARPRVACCPGMRKRTSGLPACGAAICQPPRNGSCVQ 120
QY 121 GRCCPAGMRGDTQSDVDECSARGGCPORCINTAGSYWCQMEGHSLSADGTLCPVGK 180
DB 121 GRCCPAGMRGDTQSDVDECSARGGCPORCINTAGSYWCQMEGHSLSADGTLCPVGK 180
QY 181 GPRVAPVPTGVDAMSKEEVORLSRVDLLEKQLVLAPLHSLASQALEHGLDPDPSGL 240
DB 181 GPRVAPVPTGVDAMSKEEVORLSRVDLLEKQLVLAPLHSLASQALEHGLDPDPSGL 240
QY 241 VHSFOQLGRIDLSLEQTSFLEEQIGSCSCKKDS 273
DB 241 VHSFOQLGRIDLSLEQTSFLEEQIGSCSCKKDS 273

RESULT 15
US-09-978-189-508
Sequence 508, Application US/09978189
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyere, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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Query Match 100.0%; Score 1505; DB 25; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.6e-113;

Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	181	GPPRYAPNPTGVDSAMKEEVORLQSRVLDLEKLOLVLAPLHSLASQALEHGLPDPGSLT	240	
Db	181	GPPRYAPNPTGVDSAMKEEVORLQSRVLDLEKLOLVLAPLHSLASQALEHGLPDPGSLT	240	
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Job time : 406 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:15:18 ; Search time 61 Seconds
(without alignments)
653,018 Million cell updates/sec

Title: US-09-978-191a-506

Perfect score: 1505
Sequence: 1 MNGSOEVLMLVLA VGT.....SEQISFLERQLSCSCCKXDS 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1505	100.0	273	10	US-09-978-295A-506
3	1505	100.0	273	10	US-09-978-295A-508
4	1505	100.0	273	10	US-09-978-697-506
5	1505	100.0	273	10	US-09-978-697-508
6	1505	100.0	273	10	US-09-978-192A-506
7	1505	100.0	273	10	US-09-978-192A-508
8	1505	100.0	273	10	US-09-999-832A-506
9	1505	100.0	273	10	US-09-999-832A-508
10	1505	100.0	273	11	US-09-978-189-506
11	1505	100.0	273	11	US-09-978-189-508
12	1505	100.0	273	11	US-09-978-608A-506
13	1505	100.0	273	11	US-09-978-608A-508
14	1505	100.0	273	11	US-09-978-585A-506
15	1505	100.0	273	11	US-09-978-585A-508

16	1505	100.0	273	11	US-09-978-191A-506	Sequence 506, App
17	1505	100.0	273	11	US-09-978-191A-508	Sequence 508, App
18	1505	100.0	273	11	US-09-978-403A-506	Sequence 506, App
19	1505	100.0	273	11	US-09-978-403A-508	Sequence 508, App
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21	1505	100.0	273	11	US-09-978-564A-508	Sequence 508, App
22	1505	100.0	273	11	US-09-999-833A-506	Sequence 506, App
23	1505	100.0	273	11	US-09-999-833A-508	Sequence 508, App
24	1505	100.0	273	11	US-09-981-915A-506	Sequence 506, App
25	1505	100.0	273	11	US-09-981-915A-508	Sequence 508, App
26	1505	100.0	273	11	US-09-978-824-506	Sequence 506, App
27	1505	100.0	273	11	US-09-978-824-508	Sequence 508, App
28	1505	100.0	273	11	US-09-918-585A-506	Sequence 506, App
29	1505	100.0	273	11	US-09-918-585A-508	Sequence 508, App
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31	1505	100.0	273	11	US-09-978-423A-508	Sequence 508, App
32	1505	100.0	273	11	US-09-978-193A-506	Sequence 506, App
33	1505	100.0	273	11	US-09-978-193A-508	Sequence 508, App
34	1505	100.0	273	11	US-09-999-830A-506	Sequence 506, App
35	1505	100.0	273	11	US-09-999-830A-508	Sequence 508, App
36	1505	100.0	273	11	US-09-978-757A-506	Sequence 506, App
37	1505	100.0	273	11	US-09-978-757A-508	Sequence 508, App
38	1505	100.0	273	11	US-09-978-187B-506	Sequence 506, App
39	1505	100.0	273	11	US-09-978-187B-508	Sequence 508, App
40	1505	100.0	273	11	US-09-978-643A-506	Sequence 506, App
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42	1505	100.0	273	12	US-09-978-375A-506	Sequence 506, App
43	1505	100.0	273	12	US-09-978-375A-508	Sequence 508, App
44	1505	100.0	273	12	US-09-978-188A-506	Sequence 506, App
45	1505	100.0	273	12	US-09-978-188A-508	Sequence 508, App

ALIGNMENTS

RESULT 1
US-09-790-264-10
Sequence 10, Application US/09790264
Patent No. US20020028508A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: 07334-322001
CURRENT FILING DATE: US/09/790,264
PRIOR APPLICATION NUMBER: 2001-02-21
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/298,531
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 09/065,363
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-09-790-264-10

Query Match 100.0%; Score 1505; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-978-295A-506
Sequence 506, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrera, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kijavitt, Ivay J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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 PRIOR APPLICATION NUMBER: 60/083742
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 PRIOR APPLICATION NUMBER: 60/084441
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085579
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 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.5e-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLVAVGTEHAAYRGRVCAVAGHPVSESFPQRYQPFLLTCDHR 60
 DB 1 MRGSEVLLMWLVAVGTEHAAYRGRVCAVAGHPVSESFPQRYQPFLLTCDHR 60
 QY 61 ACSTYRTTYRTAYRRSPOLAPARPRVACCPMKRTSGLPACGAACOPPCRNCGSCVQP 120
 DB 61 ACSTYRTTYRTAYRRSPOLAPARPRVACCPMKRTSGLPACGAACOPPCRNCGSCVQP 120
 QY 121 GRCRCPAGMRGDTQSDYDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTLVCPKG 180
 DB 121 GRCRCPAGMRGDTQSDYDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTLVCPKG 180
 QY 181 GPPRVAPNPTGVDSAMKEEVRLOSRYDLLEKQLVLAPLHSLASQALHEGLPDPGSL 240
 DB 181 GPPRVAPNPTGVDSAMKEEVRLOSRYDLLEKQLVLAPLHSLASQALHEGLPDPGSL 240
 QY 241 VHSFOQLGRIDSLSEQISFLEQIGSCSKCKDS 273
 DB 241 VHSFOQLGRIDSLSEQISFLEQIGSCSKCKDS 273

RESULT 3
 US-09-978-295A-508
 Sequence 508, Application US/0978295A
 Patent No. US20020156006A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630D1C11
 CURRENT FILING DATE: US/09/978, 295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585

[illegible]

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQSEVLLMLVLA VGTETAYRPRGRVCAVRAHGDVSESFVQVYTOPFLITTCGHR 60
DB 1 MRSQSEVLLMLVLA VGTETAYRPRGRVCAVRAHGDVSESFVQVYTOPFLITTCGHR 60
QY 61 ACSTYRTITRTAYRBSGGLAPARPRACCGMRTSGLGAGCAATCCPPCNGSGCVOP 120
DB 61 ACSTYRTITRTAYRBSGGLAPARPRACCGMRTSGLGAGCAATCCPPCNGSGCVOP 120
QY 121 GRCRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCEGHSLSADGTLCPVPG 180
DB 121 GRCRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCEGHSLSADGTLCPVPG 180
QY 181 GPPRAVNPPTGVDSANKEEVORIQSFVDLLEKQLVLA PLHSLASQALEHGLPDRGSL 240
DB 181 GPPRAVNPPTGVDSANKEEVORIQSFVDLLEKQLVLA PLHSLASQALEHGLPDRGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEQLGSGCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEQLGSGCKKDS 273

RESULT 4
US-09-978-697-506
Sequence 506, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1, se-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSQEVLMVLTAVNGCTSHAYRGRNCAVNAHGPVSESPYQRYQFLLTTCGHR 60
 DB 1 MGSQEVLMVLTAVNGCTSHAYRGRNCAVNAHGPVSESPYQRYQFLLTTCGHR 60
 QY 61 ACSTRTTYRTAYRRSPGLAPAPRPYACCPMKETSGLPACGAIAICPPRNGSCVOP 120
 DB 61 ACSTRTTYRTAYRRSPGLAPAPRPYACCPMKETSGLPACGAIAICPPRNGSCVOP 120
 QY 121 GRCRCPAGMRGDTQSDVDECSARRGCPQRCINTAGSYWCQWEGHSLSDGTLCPYKG 180
 DB 121 GRCRCPAGMRGDTQSDVDECSARRGCPQRCINTAGSYWCQWEGHSLSDGTLCPYKG 180
 QY 181 GPRVAPNPTGVDSMKKEVORLOSRYDLLEKXQVIAPIHSLASQALEHGLPDPSSL 240
 DB 181 GPRVAPNPTGVDSMKKEVORLOSRYDLLEKXQVIAPIHSLASQALEHGLPDPSSL 240
 QY 241 VHSFQULGRIDSLSQISFLEBOLGSCCKKDS 273
 DB 241 VHSFQULGRIDSLSQISFLEBOLGSCCKKDS 273

RESULT 5
 US-09-978-697-508
 Sequence 508, Application US/09978697
 Patent No. US20020169284A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrari, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gutney, Austin L.

APPLICANT: Hillan, Kenneth J
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31

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PRIOR APPLICATION NUMBER: 60/080334
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PRIOR APPLICATION NUMBER: 60/084366
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61  ACSTYRTIYRIARSPGLAPARPRYACCPGMRKTSGLPGAGALICPPCNGSCVOP 120
QY      121  GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCOCWEGHSLASDGTLCVPRG 180
DB      121  GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCOCWEGHSLASDGTLCVPRG 180
QY      181  GPPRVAPNPTGVDSAMKEVORLOSRYVDLLEKLOVLAPLHSLASQALEHGLPPGSL 240
DB      181  GPPRVAPNPTGVDSAMKEVORLOSRYVDLLEKLOVLAPLHSLASQALEHGLPPGSL 240
QY      241  VHSFOOLGRIDSLSEQISFLFEOLGSCSCCKDS 273
DB      241  VHSFOOLGRIDSLSEQISFLFEOLGSCSCCKDS 273

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; Sequence 506, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deshoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 ACSTYRTTYRTAYRRSPGLAPARPPYACCPGMRKTSGLPGACGAICOPPRNGSSCVQP 120
DB 61 ACSTYRTTYRTAYRRSPGLAPARPPYACCPGMRKTSGLPGACGAICOPPRNGSSCVQP 120
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121 GRCRCFAGMGRDTCQSDVDECSARRGGCPORCINTAGSYWCQCEGHSLSADGTLCPVKG 180
DB 121 GRCRCFAGMGRDTCQSDVDECSARRGGCPORCINTAGSYWCQCEGHSLSADGTLCPVKG 180
QY 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEKQLVLAFLHSLASQALEHGLDPGSL 240
181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEKQLVLAFLHSLASQALEHGLDPGSL 240
DB 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEKQLVLAFLHSLASQALEHGLDPGSL 240
QY 241 VHSFOQLGRIDSLSFOISFLEOLGSCCKKDS 273
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DB 241 VHSFOQLGRIDSLSFOISFLEOLGSCCKKDS 273

RESULT 7
US-09-978-192A-508

Sequence 508. Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Filvaroff, Ellen
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P630P1C9
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CURRENT FILING DATE: 2001-10-15
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1505; DB 10; Length 273;
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Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      1  MRGSEVLLMLLVAVGSTEHAHYRGRVCAVRAHGDVSSFPVQVYQPELTTCDDGR 60
Db      1  MRGSEVLLMLLVAVGSTEHAHYRGRVCAVRAHGDVSSFPVQVYQPELTTCDDGR 60

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      61 ACSTRTTYRTYRSPGLAPRPYACCPGKRTISGLFGACGAICPPCNGGSCVOP 120
Db      61 ACSTRTTYRTYRSPGLAPRPYACCPGKRTISGLFGACGAICPPCNGGSCVOP 120

Qy      121 GRCRCPAGRGDTCCSDVDECSARGGCPQRCINTAGSYWCOCWGHSLASAGTLCVPG 180
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Db      121 GRCRCPAGRGDTCCSDVDECSARGGCPQRCINTAGSYWCOCWGHSLASAGTLCVPG 180

Qy      181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
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; Sequence 506, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Wood, William I.
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FILE REFERENCE: P2630PIC63
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PRIOR FILING DATE: 2001-10-24
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PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRGSEVILMWLVLVAVGTEHAYRPGRRVCAYRAHGDVSESFVQRYVQPFLLTCDGHR 60
Db 1 MRGSEVILMWLVLVAVGTEHAYRPGRRVCAYRAHGDVSESFVQRYVQPFLLTCDGHR 60
Oy 61 ACSTYRTTYRATVARRSPGLAPARPVRVACCPGWRKTSGLPGACGAALCQPPCRNGSCVCP 120

Db 61 ACSTRTVIRYARRPGIAPAPRACCPGKMTSGILGACGAICQPPCHNGSCVOP 120
QY 121 GRCRCAGMRGPTCCSDVECSARRGGCPORCINTNGSGWCCWEGSHISAPGTCVPRG 180
Db 121 GRCRCAGMRGPTCCSDVECSARRGGCPORCINTNGSGWCCWEGSHISAPGTCVPRG 180
QY 181 GPPRAVNPFTGVDSAMKEEVQRLOSRFVLDLEKQLVLAPLHSLASQALEHLPDPSLL 240
Db 181 GPPRAVNPFTGVDSAMKEEVQRLOSRFVLDLEKQLVLAPLHSLASQALEHLPDPSLL 240
QY 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKDS 273
Db 241 VHSFOQLGRIDSLSEQISFLFEQLGSCCKDS 273
RESULT 9
US-09-999-832A-508
Sequence 508, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Iyar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,Se-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSQEVLLMLLVAVGSTEHAHVRGRRVCVAVRANGPVSSEFVQRYOPELITTCDSHR 60
DB 1 MRSQEVLLMLLVAVGSTEHAHVRGRRVCVAVRANGPVSSEFVQRYOPELITTCDSHR 60
QY 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGMRKRTSLPGAAGAIICPPCRNGSSCVQP 120
DB 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGMRKRTSLPGAAGAIICPPCRNGSSCVQP 120
QY 121 GRCRCPAGMRBDTCQSDVDESGARRGCGPCRCINTAGSYWCQCEGHSLSADGTLCPVKG 180
DB 121 GRCRCPAGMRBDTCQSDVDESGARRGCGPCRCINTAGSYWCQCEGHSLSADGTLCPVKG 180
QY 181 GPRVAPNPVTGVDSSMKKEEVOVLQGRVLLLEKQLVLAPLHSLASQALEHGLDPGSL 240
DB 181 GPRVAPNPVTGVDSSMKKEEVOVLQGRVLLLEKQLVLAPLHSLASQALEHGLDPGSL 240
QY 241 VHSFOQLGRIDSLSEQLSFLSEQLGSCCKXDS 273
DB 241 VHSFOQLGRIDSLSEQLSFLSEQLGSCCKXDS 273
RESULT 10
US-09-978-189-506
Sequence 506, Application US/0978189
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geider, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450

[illegible]

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 11; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLMWLVLAGVGTGTHAVRPGRRVCAVAHDDPPSESVQVYQVPLTTCGR 60
DB 1 MRGSEVLMWLVLAGVGTGTHAVRPGRRVCAVAHDDPPSESVQVYQVPLTTCGR 60

QY 61 ACSTYRTTYRTRVRRSPGLAPRRPVACCPGKRTSGLPACGALICQPPCRNGSCVCP 120
DB 61 ACSTYRTTYRTRVRRSPGLAPRRPVACCPGKRTSGLPACGALICQPPCRNGSCVCP 120

QY 121 GRCCPAGMGDTQGSVDSCSARGGCPQRCINTAGSYWCQCEGHSLSDGTLCPKG 180
DB 121 GRCCPAGMGDTQGSVDSCSARGGCPQRCINTAGSYWCQCEGHSLSDGTLCPKG 180

QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVYDLBEKTLQVLAPHSIASQALHGLPDPGSL 240
DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVYDLBEKTLQVLAPHSIASQALHGLPDPGSL 240

QY 241 VHSFOQLGRIDSLSEQISFLBEQIGSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLBEQIGSCCKKDS 273

RESULT 11
US-09-978-189-508
Sequence 508, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083500
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13

PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 11; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1,5e-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLVLANGTEHAYRPGRRVCARAHGDPVSESFVQRYQPFLLTTCGHR 60
 DB 1 MRGSEVLLMWLVLANGTEHAYRPGRRVCARAHGDPVSESFVQRYQPFLLTTCGHR 60
 QY 61 ACSTYRTTYRTAYRSPGLAPARPRVACCPGMRKTSGLPGACGAICOPPRNGSGCVP 120
 DB 61 ACSTYRTTYRTAYRSPGLAPARPRVACCPGMRKTSGLPGACGAICOPPRNGSGCVP 120
 QY 121 GRCRCPAGMRGDTQCSVDDECSARCGCPORCINTAGSYWCQCEHSLSDGTLCPYK 180
 DB 121 GRCRCPAGMRGDTQCSVDDECSARCGCPORCINTAGSYWCQCEHSLSDGTLCPYK 180
 QY 181 GPPVAPNPCTGVDSAMKEEVORLOSRYDLLEEKQLVLAPLHSLASQALEHGLDPDPSLL 240
 DB 181 GPPVAPNPCTGVDSAMKEEVORLOSRYDLLEEKQLVLAPLHSLASQALEHGLDPDPSLL 240
 QY 241 VHSFOQLGRIDSLSQISFLEQJGSCCKKDS 273
 DB 241 VHSFOQLGRIDSLSQISFLEQJGSCCKKDS 273

RESULT 12

US-09-978-608A-506
 Sequence 506, Application US/09978608A
 Publication No. US20030045462A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel

```

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 506
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-506

Query Match          100.0%; Score 1505; DB 11; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLLVLAAGTEHAAYRPGRRVCAYRAHGDVSESFVORYQPFLLTCDGHR 60
DB 1 MRGSEVLLMWLLVLAAGTEHAAYRPGRRVCAYRAHGDVSESFVORYQPFLLTCDGHR 60
QY 61 ACSTRTTYRTAYRSPGLAPAPRRYACCPGMRKTSGLPGACGAICOPPCRNSSCVOP 120
DB 61 ACSTRTTYRTAYRSPGLAPAPRRYACCPGMRKTSGLPGACGAICOPPCRNSSCVOP 120
QY 121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCBGSHLSADGTLCPVKG 180
DB 121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCBGSHLSADGTLCPVKG 180
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFQQLGRIDLSLSEQISFLLEQLGSCGCKDS 273
DB 241 VHSFQQLGRIDLSLSEQISFLLEQLGSCGCKDS 273

RESULT 13
US-09-978-608A-508
; Sequence 508, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
```

```

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 508
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-508

Query Match          100.0%; Score 1505; DB 11; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLLVLAAGTEHAAYRPGRRVCAYRAHGDVSESFVORYQPFLLTCDGHR 60
DB 1 MRGSEVLLMWLLVLAAGTEHAAYRPGRRVCAYRAHGDVSESFVORYQPFLLTCDGHR 60
QY 61 ACSTRTTYRTAYRSPGLAPAPRRYACCPGMRKTSGLPGACGAICOPPCRNSSCVOP 120
DB 61 ACSTRTTYRTAYRSPGLAPAPRRYACCPGMRKTSGLPGACGAICOPPCRNSSCVOP 120
QY 121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCBGSHLSADGTLCPVKG 180
DB 121 GRCRCPAGMRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCBGSHLSADGTLCPVKG 180
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFQQLGRIDLSLSEQISFLLEQLGSCGCKDS 273
DB 241 VHSFQQLGRIDLSLSEQISFLLEQLGSCGCKDS 273

RESULT 14
US-09-978-585A-506
; Sequence 506, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,585A
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CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 506
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-506

Query Match 100.0%; Score 1505; DB 11; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQEVLLMLLVLAAGGTEHAYRGRVCAVRAHGDVSESFVQRYVQPELTTCGHR 60
DB 1 MRSQEVLLMLLVLAAGGTEHAYRGRVCAVRAHGDVSESFVQRYVQPELTTCGHR 60
QY 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGWRKRTSGLPAGCAATCCPPCNGGSCVOP 120
DB 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGWRKRTSGLPAGCAATCCPPCNGGSCVOP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCGHSLADGTLCPKRG 180
DB 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCGHSLADGTLCPKRG 180
QY 181 GPPRYAPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRYAPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEEQSGSCCKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEEQSGSCCKDS 273

RESULT 15

US-09-978-585A-508
Sequence 508, Application US/09978585A
Publication No. US20030049633A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm

SEQ ID NO 508
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-508

Query Match 100.0%; Score 1505; DB 11; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQEVLLMLLVLAAGGTEHAYRGRVCAVRAHGDVSESFVQRYVQPELTTCGHR 60
DB 1 MRSQEVLLMLLVLAAGGTEHAYRGRVCAVRAHGDVSESFVQRYVQPELTTCGHR 60
QY 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGWRKRTSGLPAGCAATCCPPCNGGSCVOP 120
DB 61 ACSTRTTYRTAYRRSPGLAPARPRYACCPGWRKRTSGLPAGCAATCCPPCNGGSCVOP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCGHSLADGTLCPKRG 180
DB 121 GRCRCPAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCGHSLADGTLCPKRG 180
QY 181 GPPRYAPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRYAPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEEQSGSCCKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEEQSGSCCKDS 273

Search completed: September 10, 2003, 17:24:42
Job time : 63 secs

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```
Patent No. 6392018
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
FILE REFERENCE: 24011-727
CURRENT APPLICATION NUMBER: US/09/249,697A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(553)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-6
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Query Match          16.9%; Score 254.5; DB 4; Length 553;
Best Local Similarity 34.5%; Pred. No. 1.4e-12;
Matches 60; Conservative 21; Mismatches 62; Indels 31; Gaps 7;
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QY 39 PVSESPQRYVQPLTTCDGHRACSTYRTYRTAYRRSPGLAPRRVACCPGCKRTSGI 98
DB 2 PLPWSLALPLLPWVAGGFNNAASARHGLASA--RQPGVCHYGTKLAACYGMRNS-- 57
QY 99 PGACGAATCQPPCRNGSCVQPGRCRCPAGMRGDTQSDVDDECSARRGCPQRCINTAGS 158
DB 58 KGVC-EATCEPGCK-FGEICVGNKRCRCPFGYGTGKTSQDVNECGMKRPRPCQHRCVNTHGS 115
QY 159 YWCQCEGHSLSADGTLCTV-----PKGGPP-----RVAPN 188
DB 116 YKCFCLSGHMLMPDAT-CVNSRTCAMINCOYSCDETEBGPQCLCPSSGLRLAPN 168
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RESULT 3
US-09-363-316B-6
Sequence 6, Application US/09363316B
Patent No. 6392019
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Yeung, George
TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
FILE REFERENCE: 28110/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 09/249,697
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (357)
OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-6
```

```
Query Match          16.9%; Score 254.5; DB 4; Length 553;
Best Local Similarity 34.5%; Pred. No. 1.4e-12;
Matches 60; Conservative 21; Mismatches 62; Indels 31; Gaps 7;
QY 39 PVSESPQRYVQPLTTCDGHRACSTYRTYRTAYRRSPGLAPRRVACCPGCKRTSGI 98
```

```
DB 2 PLPWSLALPLLPWVAGGFNNAASARHGLASA--RQPGVCHYGTKLAACYGMRNS-- 57
QY 99 PGACGAATCQPPCRNGSCVQPGRCRCPAGMRGDTQSDVDDECSARRGCPQRCINTAGS 158
DB 58 KGVC-EATCEPGCK-FGEICVGNKRCRCPFGYGTGKTSQDVNECGMKRPRPCQHRCVNTHGS 115
QY 159 YWCQCEGHSLSADGTLCTV-----PKGGPP-----RVAPN 188
DB 116 YKCFCLSGHMLMPDAT-CVNSRTCAMINCOYSCDETEBGPQCLCPSSGLRLAPN 168
```

```
RESULT 4
US-09-312-283C-389
Sequence 389, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Murist, Rene
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 389
LENGTH: 284
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-389
```

```
Query Match          16.8%; Score 252.5; DB 4; Length 284;
Best Local Similarity 36.3%; Pred. No. 9.3e-13;
Matches 53; Conservative 15; Mismatches 51; Indels 27; Gaps 4;
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```
QY 66 RTTYRTAYRRSPGLAPRRVACCPGCKRTSGIPLPGACGAATCQPPCRNGSCVQPGRCRC 125
DB 47 RDYMLPALAHQPGVCHYGTKTAACYGMRNS--KGVC-EAVCEPRCK-FGEICVGNKRCRC 102
QY 126 PAGMRGDTQSDVDDECSARRGCPQRCINTAGSYWCQCEGHSJ----- 169
DB 103 PFGYGTGKTSQDVNECGMKRPRPCQHRCVNTHGSYKCFCLSGHMLLPATCSNSRTCARIN 162
QY 170 -----SADGTLCTVCPKGGPPRVAPN 188
DB 163 COYSCDETEBGPQCLCPSSGLRLAPN 188
```

```
RESULT 5
US-09-249-697A-19
Sequence 19, Application US/09249697A
Patent No. 6392018
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Yeung, George
TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
FILE REFERENCE: 24011-727
CURRENT APPLICATION NUMBER: US/09/249,697A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-249-697A-19
```

```

Query Match          16.7%; Score 251.5; DB 4; Length 553;
Best Local Similarity 36.8%; Pred. No. 2,4e-12;
Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7

Oy 58 GHRACSTYRTTYRTAYRRSPGLAPAPRRYACCPGWRKRTSGLPAGCAATCOPPCRNNGSC 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 GNAASARHHGLLASA--RQPGVCHYGTKLACCYGMRRNS--KGVG-EATCEPGCK-FGBC 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 118 VQPGRCRCPAGMRGDTCCSDVDECSARRGGCTFORCINTAGSYWCOCWEGHSI.SADGTLGV 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 VGPNNKRCRFPFGYTGTCSDVNECGMKRPRCOHRCVNTHGSIKCYCLSGHMLMPDAT-CV 133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 178 -----PKGPP-----RVAPN 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 NSRTCAMINCOYSCDTEBGPCLCPSSGLRLAPN 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-09-363-316B-24
; Sequence 24, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Yeung, John
; APPLICANT: Ford, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-363-316B-24

Query Match          16.7%; Score 251.5; DB 4; Length 553;
Best Local Similarity 36.8%; Pred. No. 2,4e-12;
Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7

Oy 58 GHRACSTYRTTYRTAYRRSPGLAPAPRRYACCPGWRKRTSGLPAGCAATCOPPCRNNGSC 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 GNAASARHHGLLASA--RQPGVCHYGTKLACCYGMRRNS--KGVG-EATCEPGCK-FGBC 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 118 VQPGRCRCPAGMRGDTCCSDVDECSARRGGCTFORCINTAGSYWCOCWEGHSI.SADGTLGV 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 VGPNNKRCRFPFGYTGTCSDVNECGMKRPRCOHRCVNTHGSIKCYCLSGHMLMPDAT-CV 133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 178 -----PKGPP-----RVAPN 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 NSRTCAMINCOYSCDTEBGPCLCPSSGLRLAPN 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-363-316B-18
; Sequence 18, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22

```

```

/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 18
/ LENGTH: 502
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (501-502)
/ OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-18

Query Match
Best Local Similarity 14.4%; Score 216.5; DB 4; Length 502;
Matches 48; Conservative 10; Mismatches 35; Indels 29; Gaps 6;

QY 91 GWKRTSLPGACGAALICPPCRNGSCVQPGRCRCPAGWRGDTCSQDVDECSARRGGCPQ 150
DB 1 GWRNRS--KGVC-EATCEPGCK-FGECEVGNKRCRCPGYTGKTCSDQDVNECGMKRPPCQH 56
QY 151 RCINTAGSYWCQCEGHSLSADGTLV-----PKGPP-----RVA 186
DB 57 RCVNTHGSYKCFCLSGHMLMPDAT-CVNSRTCAMINCYSCEDTBEGPCLCPSSGLRLA 115
QY 187 PN 188
DB 116 PN 117

RESULT 8
US-09-249-697A-4
/ Sequence 4, Application US/09249697A
/ Patent No. 6392018
/ GENERAL INFORMATION:
/ APPLICANT: Ford, John
/ APPLICANT: Yeung, George
/ TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
/ FILE REFERENCE: 24011-727
/ CURRENT APPLICATION NUMBER: US/09/249,697A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 08/968,800
/ PRIOR FILING DATE: 1997-11-22
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 537
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(537)
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-4

Query Match
Best Local Similarity 14.4%; Score 216.5; DB 4; Length 537;
Matches 48; Conservative 10; Mismatches 35; Indels 29; Gaps 6;

QY 91 GWKRTSLPGACGAALICPPCRNGSCVQPGRCRCPAGWRGDTCSQDVDECSARRGGCPQ 150
DB 1 GWRNRS--KGVC-EATCEPGCK-FGECEVGNKRCRCPGYTGKTCSDQDVNECGMKRPPCQH 56
QY 151 RCINTAGSYWCQCEGHSLSADGTLV-----PKGPP-----RVA 186
DB 57 RCVNTHGSYKCFCLSGHMLMPDAT-CVNSRTCAMINCYSCEDTBEGPCLCPSSGLRLA 115
QY 187 PN 188
DB 116 PN 117

RESULT 9

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Db 250 PEGHSTFHLCLCPGFTGLDCENMPD 275

RESULT 13

US-08-282-141-2
Sequence 2, Application US/08282141
Patent No. 5538861
GENERAL INFORMATION:
APPLICANT: Schneider, Claudio
APPLICANT: Varnum, Brian
APPLICANT: Avanzi, Giancarlo
APPLICANT: Brancolini, Claudio
APPLICANT: Manfioletti, Guidalberto
TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,141
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-282-141-2

Query Match 12.6%; Score 189; DB 1; Length 678;
Best Local Similarity 34.2%; Pred. No. 2.9e-07;
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Qy 46 QRYVQPELTTCDGH-----RACSTYRTYTRAVRSPGLAPARRVACC-----PGWK 93
Db 47 RAQVQFEBAKQGHLEKCEVELCS--REAREVEFNDPDTDYFYPRYLDCKINKYGSPT 104
Qy 94 RTSG-----LPGACGAALICQPPC-RNGSCVOP--GR--CRCPAGRGDTCCQSDVDEC 141
Db 105 KNSGFATCVQNLPPDC---TNPFCDRKGTQACQDLMGNFLLCAGMGRLCDKDVNEC 160
Qy 142 SARRGCCPQRCINTAGSYWCQCQWEGHSLADGTLIC 176
Db 161 SOENGGLQICHNKPGSFHCSHSGFELSSDGRTC 195

RESULT 14

US-08-435-434-2
Sequence 2, Application US/08435434
Patent No. 5714385
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,434
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-434-2

Query Match 12.6%; Score 189; DB 1; Length 678;
Best Local Similarity 34.2%; Pred. No. 2.9e-07;
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Qy 46 QRYVQPELTTCDGH-----RACSTYRTYTRAVRSPGLAPARRVACC-----PGWK 93
Db 47 RAQVQFEBAKQGHLEKCEVELCS--REAREVEFNDPDTDYFYPRYLDCKINKYGSPT 104
Qy 94 RTSG-----LPGACGAALICQPPC-RNGSCVOP--GR--CRCPAGRGDTCCQSDVDEC 141
Db 105 KNSGFATCVQNLPPDC---TNPFCDRKGTQACQDLMGNFLLCAGMGRLCDKDVNEC 160
Qy 142 SARRGCCPQRCINTAGSYWCQCQWEGHSLADGTLIC 176
Db 161 SOENGGLQICHNKPGSFHCSHSGFELSSDGRTC 195

RESULT 15

US-08-435-436-2
Sequence 2, Application US/08435436
Patent No. 5721139
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 946-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 678 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
US-08-435-436-2

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Query Match 12.6%; Score 189; DB 1; Length 678;
Best Local Similarity 34.2%; Pred. No. 2.9e-07;
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

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QY 46 QRYVQPLTICDGH-----RAGSTYRTYRTAYRSFGLAPARPRYACC-----PGWK 93
Db 47 RRAQVFEBAKQGLERECEVEELCS--REAREVFENDPETDYFFPRYLDICINKYSPYT 104
QY 94 RTSG-----LPAGCGAICQPPC--RNGGSCVQP--GR--CRCPAGMRGDTGQSDVDEC 141
Db 105 KNSGFATCVQNLDPQC-----TPNPCDRKGTQACODLMGNFFCLCKAGMGRLCDKDYNEC 160
QY 142 SARRGCCPQRCINTAGSYWCQCWEHSLADGTLG 176
Db 161 SOENGGLQICHNKPGSFHCCHSGFELSSDGRTC 195

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Search completed: September 10, 2003, 17:16:13
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 10, 2003, 17:02:48 ; Search time 85 Seconds
(without alignments)
509.792 Million cell updates/sec

Title: US-09-978-191a-506
Perfect score: 1505
Sequence: 1 MKGSEVLIMLVLAVAGT.....SEQISLEBQLGSCSKKDS 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	100.0	273	20	AAV41769
2	1505	100.0	273	20	AAV41770
3	1505	100.0	273	21	AAAB4325
4	1505	100.0	273	21	AAAB4326
5	1505	100.0	273	21	AAAB18673
6	1505	100.0	273	21	AAAB18674
7	1505	100.0	273	21	AAAB24042
8	1505	100.0	273	21	AAAB24043
9	1505	100.0	273	21	AAV52137

10	1505	100.0	273	23	AAE21079
11	1505	100.0	273	23	AAU83680
12	1505	100.0	273	24	ABU61155
13	1505	100.0	273	24	ABU61156
14	1504	99.9	273	20	AAV41771
15	1504	99.9	273	20	AAW88381
16	1504	99.9	273	21	AAAB4327
17	1504	99.9	273	21	AAAB4327
18	1504	99.9	273	21	AAAB18675
19	1504	99.9	273	21	AAAB24044
20	1504	99.9	273	21	AAAB01376
21	1504	99.9	273	22	AAW23991
22	1504	99.9	273	22	AAAB61509
23	1504	99.9	273	24	ABU61157
24	1410	93.7	254	20	AAW88382
25	1393	92.6	251	23	AAE21080
26	1341.5	89.1	295	20	AAV41685
27	1341.5	89.1	295	21	AAAB44241
28	1341.5	89.1	295	23	ABW95609
29	1341.5	89.1	295	24	ABW85003
30	1280	85.0	307	21	ABU61071
31	1251.5	83.2	234	22	AAU00397
32	1236	82.1	224	20	AAV59870
33	1180	78.4	275	21	AAV52141
34	1180	78.4	275	23	AAE21081
35	1180	78.4	278	20	AAW88392
36	1180	78.4	278	22	AAE05356
37	1138.5	75.6	255	20	AAW88397
38	1099	73.0	265	21	AAAB42204
39	1073	71.3	255	23	ABW72368
40	944.5	62.8	287	22	AAU16977
41	944.5	62.8	288	22	ABW10533
42	944.5	62.8	288	22	AAU18135
43	944.5	62.8	288	22	AAU17049
44	944.5	62.8	288	22	AAU19910
45	944.5	62.8	288	23	ABP67120

ALIGNMENTS

RESULT 1	AAV41769	AAV41769 standard; Protein; 273 AA.
ID	AAV41769;	
AC	AAV41769;	
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DT	07-DEC-1999 (first entry)	
XX		
DE	Human PRO213-1 protein sequence.	
XX		
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
XX	secreted protein; transmembrane protein.	
OS	Homo sapiens.	
XX		
FN	W09946281-A2.	
XX		
PD	16-SEP-1999.	
XX		
PF	08-MAR-1999;	99WO-US05028.
XX		
PR	10-MAR-1998;	98US-0077450.
PR	11-MAR-1998;	98US-0077632.
PR	11-MAR-1998;	98US-0077641.
PR	11-MAR-1998;	98US-0077649.
PR	12-MAR-1998;	98US-0077791.
PR	13-MAR-1998;	98US-0078004.
PR	17-MAR-1998;	98US-0040220.
PR	20-MAR-1998;	98US-0078866.
PR	20-MAR-1998;	98US-0078910.
PR	20-MAR-1998;	98US-0078936.

Human T125 (TANGO-	
Human PRO protein,	
Human PRO213-1 pol	
Human PRO1330 poly	
Human PRO1449 prot	
Human neuro-growth	
Human PRO1449 prot	
Amino acid sequenc	
Human PRO1449 prot	
Neuron-associated	
Human EST encoded	
Human protein HP03	
Human PRO1449 poly	
Human neuro-growth	
Human T125 (TANGO-	
Human PRO213 prote	
Human anglogenesis	
Human PRO1449 prot	
Human PRO213 polyp	
Human ORFX ORF108	
Human secreted pro	
Human normal uteru	
Mouse T125 (TANGO-	
Mouse neuro-growth	
Mouse neuro-growth	
Mouse Notch4-like	
Mouse neuro-growth	
Human ORFX ORF198	
Murine protein iso	
Human novel secret	
Human cDNA SEQ ID	
Novel human uterin	
Human novel secret	
Novel human calcitn	
Human polypeptide	

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PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
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PR 27-MAR-1998; 98US-0079669.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
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PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
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PR 09-APR-1998; 98US-0081195.
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PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.

PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
XX
DR N-PSDB; AA234311.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
XX
PS adhesion disorders -
XX
XX
XX Claim 12; Fig 213; 530pp; English.
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA23438, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
XX
XX invention.
XX
XX Sequence 273 AA:
SQ
Query Match 100.0%; Score 1505; DB 20; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLLVLAAGTEHAHVRPGRVCAVAHAGDPVSESFVQVYOFELTTCGHR 60
DB 1 MRGSEVLLMWLLVLAAGTEHAHVRPGRVCAVAHAGDPVSESFVQVYOFELTTCGHR 60
QY 61 ACSTYRTITRYTAYRRSPGLAPARPRVACCPGKRTSGLPAGCAIICOPCRNGSCVOP 120
DB 61 ACSTYRTITRYTAYRRSPGLAPARPRVACCPGKRTSGLPAGCAIICOPCRNGSCVOP 120
QY 121 GRCPGAGMRGDTQOSVDDECSARRGCGPCQICITTAGSYWCQCEGHSLSADGTLCPYKG 180
DB 121 GRCPGAGMRGDTQOSVDDECSARRGCGPCQICITTAGSYWCQCEGHSLSADGTLCPYKG 180
QY 181 GPPRYAPNPTGVDSAMKEVORLQSRVDLLEKQLVLAFLHSLSAQLAHEGLPDPGSL 240
DB 181 GPPRYAPNPTGVDSAMKEVORLQSRVDLLEKQLVLAFLHSLSAQLAHEGLPDPGSL 240
QY 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEQLGSCCKKDS 273

RESULT 2
AA41770
ID AA41770 standard; Protein; 273 AA.
AC AA41770;
XX
XX 07-DEC-1999 (first entry)
XX
XX Human PRO1330 protein sequence.
DE
XX
XX Human; PRO: EST: expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX
XX Homo sapiens.

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RESULT 3
AAB44325
ID AAB44325 standard; Protein; 273 AA.
XX
AC AAB44325;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO213-1 protein sequence SEQ ID NO:506.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78585.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
XX Claim 12; Fig 213; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 5,5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSEVLLMVLVLAAGTETHAHPGRVCAVRHAGPVSFPQRYOPEPLTTCDHR 60
DB 1 MRGSEVLLMVLVLAAGTETHAHPGRVCAVRHAGPVSFPQRYOPEPLTTCDHR 60
QY 61 ACSTYRTTYRTAARRSPGLAPAPRRYACCPGKRTSGLPAGCAAIICPPRRNGSSCYQP 120
DB 61 ACSTYRTTYRTAARRSPGLAPAPRRYACCPGKRTSGLPAGCAAIICPPRRNGSSCYQP 120
QY 121 GECRCPAGKRGDTCCSDVDECGARRGGCPQRCINTAGSYWCQCEGHSLSADGTLVCPKG 180
DB 121 GECRCPAGKRGDTCCSDVDECGARRGGCPQRCINTAGSYWCQCEGHSLSADGTLVCPKG 180
QY 181 GPPRYAPNPTGVDSAMKEEVOQLGRVLDLEBKQLVLAPLHSLASQALEHGLDPGSL 240
DB 181 GPPRYAPNPTGVDSAMKEEVOQLGRVLDLEBKQLVLAPLHSLASQALEHGLDPGSL 240
QY 241 VHSFOQLGRIDLSLEQISFLEBOLGSCCKKDS 273
DB 241 VHSFOQLGRIDLSLEQISFLEBOLGSCCKKDS 273
RESULT 4
AAB44326
ID AAB44326 standard; Protein; 273 AA.
XX
AC AAB44326;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO1330 protein sequence SEQ ID NO:508.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 16-DEC-1999; 99WO-US28555.
XX 30-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX


```

Db 61 ACSTYRTIYRTAYRRSPGLAPARPRVACCPGMRKTSGLPGACGAICQPPCRNGSSCVQP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPRCINTAGSYWCQCEGHSLSADGTLCPYK 180
Db 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPRCINTAGSYWCQCEGHSLSADGTLCPYK 180
QY 181 GPPRYAHPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
Db 181 GPPRYAHPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDLSLSEQISFLEQLGSCGCKKDS 273
Db 241 VHSFOQLGRIDLSLSEQISFLEQLGSCGCKKDS 273

RESULT 6
AAB18674
ID AAB18674 standard; Protein: 273 AA.
AC AAB18674;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human PRO1330 polypeptide.
XX
KW Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO213; PRO1449;
KW angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;
KW atherosclerosis; cardiac hypertrophy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
FT 1..19 Location/Qualifiers
FT /note= "signal sequence"
FT 19..25 /note= "N-myristoylation site"
FT 26..30 /note= "amidation site"
FT 78..84 /note= "N-myristoylation site"
FT 93..97 /note= "N-myristoylation site"
FT /note= "CaM- and cGMP-dependent protein kinase phosphorylation site"
FT 97..103 /note= "N-myristoylation site"
FT 100..106 /note= "N-myristoylation site"
FT 103..109 /note= "N-myristoylation site"
FT 123..135 /note= "N-myristoylation site"
FT 130..133 /note= "EGF-like domain cysteine pattern signature"
FT 152..164 /note= "cell attachment sequence"
FT /note= "aspartic acid and asparagine hydroxylation site"
FT 157..163 /note= "N-myristoylation site"
FT 191..197 /note= "N-myristoylation site"
FT 265..271 /note= "N-myristoylation site"
FT /note= "N-myristoylation site"
XX
PN WO200053752-A2.
XX
PD 14-SBP-2000.
XX
PF 30-DEC-1999; 99WO-US31274.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 21-APR-1999; 99US-0130232.
PR 26-APR-1999; 99US-0131022.
PR 28-APR-1999; 99US-0131445.

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PR 14-MAY-1999; 99US-0134287.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;
PI Wood WI;
XX
DR WPI; 2000-638138/61.
DR N-PSDB; AAA75703.
XX
PT A composition useful for treatment and diagnosis of a cardiovascular,
PT endothelial or angiogenic disorder, especially cancer, comprises (an
PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,
PT PRO1330 or PRO1449 polypeptide -
XX
XX Claim 67; Fig 12; 152pp; English.
XX
PS
XX
CC The present sequence represents PRO1330, a human notch 4 homologue.
CC The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,
CC PRO1330 and PRO1449 polypeptides. The polypeptides promoter or
CC inhibit angiogenesis and cardiovascularisation in mammals. The
CC polypeptides are used for the treatment and diagnosis of a
CC cardiovascular, endothelial or angiogenic disorder, especially
CC cancer. Disorders that can be diagnosed, treated or prevented by
CC the polypeptides of the invention include trauma such as wounds,
CC atherosclerosis, and cardiac hypertrophy.
XX
SQ Sequence 273 AA;
XX
Query Match 100.0%; Score 1505; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSQSEVLMLVLAVGCTHAYRPGRRVCAVRAHGPVSESFVQRYQPFLLTCGHR 60
Db 1 MRSQSEVLMLVLAVGCTHAYRPGRRVCAVRAHGPVSESFVQRYQPFLLTCGHR 60
QY 61 ACSTYRTIYRTAYRRSPGLAPARPRVACCPGMRKTSGLPGACGAICQPPCRNGSSCVQP 120
Db 61 ACSTYRTIYRTAYRRSPGLAPARPRVACCPGMRKTSGLPGACGAICQPPCRNGSSCVQP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPRCINTAGSYWCQCEGHSLSADGTLCPYK 180
Db 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPRCINTAGSYWCQCEGHSLSADGTLCPYK 180
QY 181 GPPRYAHPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
Db 181 GPPRYAHPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDLSLSEQISFLEQLGSCGCKKDS 273
Db 241 VHSFOQLGRIDLSLSEQISFLEQLGSCGCKKDS 273

RESULT 7
AAB24042
ID AAB24042 standard; Protein: 273 AA.
AC AAB24042;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO213 protein sequence SEQ ID NO:4.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
KW tumourigenesis; detection; neoplastic cell growth; proliferation;
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200053754-A1.

```

XX 14-SEP-2000.
PD AAB24043
XX 06-JAN-2000; 2000MO-US00277.
PF
XX 08-MAR-1999; 99MO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 05-OCT-1999; 99MO-US23089.
PR 30-NOV-1999; 99MO-US28313.
PR 02-DEC-1999; 99MO-US28551.
PR 02-DEC-1999; 99MO-US28564.
PR 30-DEC-1999; 99MO-US31243.
XX 30-DEC-1999; 99MO-US31274.
XX
PA (GENTH) GENENTECH INC.
XX Baker KP, Desauvage FU, Goddard A, Gurney AL, Klein RD, Roy MA;
PI Wood WI;
XX
XX WPI: 2000-572269/53.
DR N-PSDB; AAC58226.
XX
XX New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment -
XX
XX Claim 61; Fig 4; 195pp; English.
XX
XX The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO3664, PRO618,
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
CC and methods for the diagnosis and treatment of neoplastic cell growth
CC and proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumor cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumor treatment. Compounds
CC that inhibit the expression or activity of the identified polypeptides
CC can be identified and used as antagonists. Benign or malignant tumours,
CC inflammatory disorders and immunological disorders can be treated.
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX Sequence 273 AA;
SQ

Query Match 100.0%; Score 1505; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQSEVLLMWLVLAVGSTEHAHYRGRVCAVRAHGDVSSFFVQVYQPLTTCDDGR 60
DB 1 MRSQSEVLLMWLVLAVGSTEHAHYRGRVCAVRAHGDVSSFFVQVYQPLTTCDDGR 60
QY 61 ACSTRTTITRTYRSPGLAPRPYACCPGKWRISGLFGACGAACOPPCNGSCVOP 120
DB 61 ACSTRTTITRTYRSPGLAPRPYACCPGKWRISGLFGACGAACOPPCNGSCVOP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGGCFQRCINTAGSYWCQMGHSLASAGTLCVPRG 180
DB 121 GRCRCPAGMRGDTCCSDVDECSARRGGCFQRCINTAGSYWCQMGHSLASAGTLCVPRG 180
QY 181 GPPRYAHPNTGVDSAMKEEVQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDPGSL 240
DB 181 GPPRYAHPNTGVDSAMKEEVQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOOLGRIDLSLEQISFLEBOLGSCCKKDS 273
DB 241 VHSFOOLGRIDLSLEQISFLEBOLGSCCKKDS 273

RESULT 8
AAB24043
ID AAB24043 standard; Protein; 273 AA.
XX
XX AAB24043;
XX
XX 25-JAN-2001 (first entry)
XX
XX Human PRO1330 protein sequence SEQ ID NO.6.
XX
XX Human; tumour; diagnosis; neoplastic disease; identification; cancer;
XX tumorigenesis; detection; neoplastic cell growth; proliferation;
XX cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
XX immunological disorder.
XX
XX Homo sapiens.
XX
XX WO200053754-A1.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000MO-US00277.
XX
XX 08-MAR-1999; 99MO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 05-OCT-1999; 99MO-US23089.
XX 30-NOV-1999; 99MO-US28313.
XX 02-DEC-1999; 99MO-US28551.
XX 02-DEC-1999; 99MO-US28564.
XX 30-DEC-1999; 99MO-US31243.
XX 30-DEC-1999; 99MO-US31274.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Desauvage FU, Goddard A, Gurney AL, Klein RD, Roy MA;
XX Wood WI;
XX
XX WPI: 2000-572269/53.
XX N-PSDB; AAC58227.
XX
XX New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment -
XX
XX Claim 61; Fig 6; 195pp; English.
XX
XX The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO3664, PRO618,
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
CC and methods for the diagnosis and treatment of neoplastic cell growth
CC and proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumor cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumor treatment. Compounds
CC that inhibit the expression or activity of the identified polypeptides
CC can be identified and used as antagonists. Benign or malignant tumours,
CC inflammatory disorders and immunological disorders can be treated.
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX Sequence 273 AA;
SQ

Query Match 100.0%; Score 1505; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Domain
141..176
/note="Epidermal growth factor domain 2"
US2002028508-A1.
07-MAR-2002.
21-FEB-2001; 2001US-0790264.
23-APR-1998; 98US-0065363.
23-APR-1998; 98US-0065661.
22-JUN-1998; 98US-0102705.
29-JUL-1998; 98US-0124538.
23-APR-1999; 99US-0298531.
22-JUN-1999; 99US-0337930.
29-JUL-1999; 99US-0363630.
(HOLT/) HOLTZMAN D A.
(GOOD/) GOODEARTL A D J.
(MCCA/) MCCARTHY S A.
Holtzman DA, Goodearl ADJ, McCarthy SA;
WPI: 2002-303420/34.
N-PDB; AAD33536.
Novel TANGO polypeptides and nucleic acid molecules useful as
modulating agents in regulating cellular processes and for diagnosing
and treating heart, liver, lung, kidney, inflammatory and cellular
proliferative disorders -
claim 51; Fig 4; 138pp; English.

```

50 Sequence 273 AA;
Query Match 100.0%; Score 1505; DB 23; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRGSEVLLMMLLVAVGTEHAHYPGRVCVRAHAGDPVSEFVQRYOPELITTCDAHR 60

```

Dd		1	MGSQEVLLMVLMLVLAAGSTEAHYRGRVCAYFAHGDPIVSESFQVRVVQPELITTCGHR	60
Oy		61	ACSTRTTIRTYRRSPGLAPRAPRPACCPCMKRTSTGLPGACCAAIICPPCRNGGSCVP	120
Dd		61	ACSTRTTIRTYRRSPGLAPRAPRPACCPCMKRTSTGLPGACCAAIICPPCRNGGSCVP	120
Oy		121	GRCRPCAGRGDTCCSDVDEGCASARGGCCPQCINTAGSYWCOCWEGHSLSADGTLCPKG	180
Dd		121	GRCRPCAGRGDTCCSDVDEGCASARGGCCPQCINTAGSYWCOCWEGHSLSADGTLCPKG	180
Oy		181	GPRVAHPNPTGVDSAMKEEVRQLQSRVDLLEKLTQLVLAPLSLAQALETGLPDPSLL	240
Dd		181	GPRVAHPNPTGVDSAMKEEVRQLQSRVDLLEKLTQLVLAPLSLAQALETGLPDPSLL	240
Oy		241	VHSFOQLGRIDLSLEQISFLFEQLGSCSCKXDS	273
Dd		241	VHSFOQLGRIDLSLEQISFLFEQLGSCSCKXDS	273
<hr/>				
RESULT 11				
AAU83680	ID	AAU83680 standard; Protein; 273 AA.		
XX	AC	AAU83680;		
XX	DT	08-MAY-2002 (first entry)		
XX	DE	Human PRO protein, Seq ID No 178.		
KM		Human; secreted protein; PRO; tumour; lung cancer; colon cancer;		
KM		breast cancer; prostate tumour; rectal tumour; liver tumour;		
KM		perticyte cell proliferation; chondrocyte cell proliferation;		
KM		tumour necrosis factor-alpha.		
OS		Homo sapiens.		
PN		WO200208286-A2.		
PD		31-JAN-2002.		
Pf		29-JUN-2001; 2001WO-US21066.		
PR		20-JUL-2000; 2000US-219556P.		
PR		25-JUL-2000; 2000US-220585P.		
PR		25-JUL-2000; 2000US-220605P.		
PR		25-JUL-2000; 2000US-220607P.		
PR		25-JUL-2000; 2000US-220624P.		
PR		25-JUL-2000; 2000US-220638P.		
PR		25-JUL-2000; 2000US-220664P.		
PR		26-JUL-2000; 2000US-220693P.		
PR		28-JUL-2000; 2000OMO-US20710.		
PR		23-AUG-2000; 2000OMO-US23522.		
PR		24-AUG-2000; 2000OMO-US23328.		
PR		15-SEP-2000; 2000US-000000P.		
PR		10-NOV-2000; 2000OMO-US30873.		
PR		28-NOV-2000; 2000OMO-US3646P.		
PR		01-DEC-2000; 2000OMO-US32678.		
PR		20-DEC-2000; 2000US-074725J.		
PR		20-DEC-2000; 2000OMO-US34956.		
PR		28-FEB-2001; 2001WO-US06520.		
PR		10-MAY-2001; 2001US-0854280.		
PR		25-MAY-2001; 2001WO-US17092.		
PA		(GETH) GENENTECH INC.		
XX		Baker KP, Desnoyers J, Gerritsen ME, Goddard A, Godowski PJ,		
XX		Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,		
XX		WPI; 2002-172001/22.		
DR		N-Psdb; ABK33624.		
XT		One hundred and twenty two nucleic acids encoding PRO polypeptides,		

PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
tumour or liver tumour -
XX
PS Claim 11; Figure 178; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor- α from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 273 AA;
Query Match. 100.0%; Score 1505; DB 23; Length 273;
Best Local Similarity 100.0%; Pred. No.5.5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSEVLLMMLVLAVGTEHAYRPGRRVCAVRAHGDVSESFVQRYQPFLLTCDGHR 60
Db 1 MRGSEVLLMMLVLAVGTEHAYRPGRRVCAVRAHGDVSESFVQRYQPFLLTCDGHR 60
QY 61 ACSTYRTTYTARRRSPGLAPARPRYACCPGWRKTSGLPACGAALCOPPCRNNGSCVOP 120
Db 61 ACSTYRTTYTARRRSPGLAPARPRYACCPGWRKTSGLPACGAALCOPPCRNNGSCVOP 120
QY 121 GRGCRPAGMRGDTQSDVDCEGSRARGGCPORCINTGAGSYWCQCEGHSADDTLCPVPG 180
Db 121 GRGCRPAGMRGDTQSDVDCEGSRARGGCPORCINTGAGSYWCQCEGHSADDTLCPVPG 180
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLLQVLAPLHSLASQALEHGLPDPGSL 240
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLLQVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273
Db 241 VHSFOOLGRIDSLSEQISFLEBOLGSCCKKDS 273
RESULT 12
ABU61155
ID ABU61155 standard; Protein; 273 AA.
XX
AC ABU61155;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO213-1 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antitretic; anti-tumour; vulnetary; antinaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
OS US2002169284-A1.
XX
PN 14-NOV-2002.
PD

XX 16-OCT-2001; 2001US-0978697.
XX
XX 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00217.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-079339P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 30-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 26-MAY-1981; 81US-026721P.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.

PR 10-MAR-1999; 99US-0265686.
 PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380142.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.

(GERTH) GENENTECH INC.

PI Ashkenazi A, Baker KP, Borstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

WPI: 2003-288163/28.
 N-PSDB; ABX92683.

PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies

XX Claim 12; Fig 213; 459pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC ABU61071-ABU61164 represent the human PRO polypeptides of the
 CC invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipside.htm.

XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 24; Length 273;
 Best Local Similarity 100.0%; Pred No. 5.5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQSEVLLMLLVAVGSTEHAYPEGRVCAVRAHGDVSSFPVQVYQPLITCDGR 60
 Db 1 MRSQSEVLLMLLVAVGSTEHAYPEGRVCAVRAHGDVSSFPVQVYQPLITCDGR 60
 QY 61 ACSTRTTITRTYRSPGLAPRPRACCPGKRTSTGLGAGAAICQPPCRNGSGCVOP 120
 Db 61 ACSTRTTITRTYRSPGLAPRPRACCPGKRTSTGLGAGAAICQPPCRNGSGCVOP 120

QY 121 GRCRCPAGNRGDTQSDVDECSARRGCGPQRCINTAGSYWCQCEGHSLSADGTLCPKG 180
 Db 121 GRCRCPAGNRGDTQSDVDECSARRGCGPQRCINTAGSYWCQCEGHSLSADGTLCPKG 180
 QY 181 GPPRVAPNPTGVDSAMKEVQVRLQSRVDLLEKTLQVLAPLHSLASQALEHGLPDPGSL 240
 Db 181 GPPRVAPNPTGVDSAMKEVQVRLQSRVDLLEKTLQVLAPLHSLASQALEHGLPDPGSL 240
 QY 241 VHSFOQLGRIDSLSEQISFLEQLGSCGCKDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLEQLGSCGCKDS 273

RESULT 13

ABU61156
 ID ABU61156 standard; Protein; 273 AA.

XX ABU61156;

DT 08-MAY-2003 (first entry)

XX Human PRO1330 polypeptide.

XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytoskeletal; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnerability; antineoplastic; dermatological;
 KW cardiacant.

OS Homo sapiens.

PN US2002169284-A1.

PD 14-NOV-2002.

PF 16-OCT-2001; 2001US-0978697.

XX 07-OCT-1998; 98WO-US21141.
 PR 20-NOV-1998; 98WO-US24855.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US28565.
 PR 30-DEC-1999; 99WO-US310095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US23678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 22-MAR-2001; 2001WO-US09552.
 PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19682.
PR 28-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 12-MAR-1998; 98US-077649P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078866P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079922P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 06-NOV-1998; 98US-0184216.
PR 07-DEC-1998; 98US-0187368.
PR 22-DEC-1998; 98US-0202054.
PR 05-MAR-1999; 99US-0218517.
PR 10-MAR-1999; 99US-0254465.
PR 12-APR-1999; 99US-0265686.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882536.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,
PI Ferreira N, Filvarsoff E, Fong S, Gao W, Gerber H, Gerritsen ME,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Kijavitt J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR MPI; 2003-288163/28.
DR N-PSDB; AEX92684.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
XX Claim 12; Fig 215; 459P; English.
XX
CC The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney diseases,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC AB061071-AB061164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdidentry.html.
CC
XX
SQ Sequence 273 AA;
Query Match 100.0%; Score 1505; DB 24; Length 273;
Best Local Similarity 100.0%; Pred. No. 5-5e-95;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLLVAVGTEHAYRGRVCAVRAHGDVSESFVQRYOPELITTCGHR 60
1 MRGSEVLLMLLVAVGTEHAYRGRVCAVRAHGDVSESFVQRYOPELITTCGHR 60
DB 61 AGSTRRTYRTAYRRSPGLAARPRYACCPGKRRSGPGACGAATCCPPCNGSCVOP 120
61 AGSTRRTYRTAYRRSPGLAARPRYACCPGKRRSGPGACGAATCCPPCNGSCVOP 120
DB 61 ACSTRRTYRTAYRRSPGLAARPRYACCPGKRRSGPGACGAATCCPPCNGSCVOP 120
QY 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPORCINTAGSGYWCQMGHSLADGTLCPKRG 180
121 GRCRCPAGMRGDTCCSDVDECSARRGGCPORCINTAGSGYWCQMGHSLADGTLCPKRG 180
DB 121 GRCRCPAGMRGDTCCSDVDECSARRGGCPORCINTAGSGYWCQMGHSLADGTLCPKRG 180
QY 181 GPRVAPNPTGVDSAMKEEVORLOSRLVDLEBKQLVLAPLHSLASQALEHGLPDPSGLL 240
181 GPRVAPNPTGVDSAMKEEVORLOSRLVDLEBKQLVLAPLHSLASQALEHGLPDPSGLL 240
DB 181 GPRVAPNPTGVDSAMKEEVORLOSRLVDLEBKQLVLAPLHSLASQALEHGLPDPSGLL 240
QY 241 VHSFOQLGRIDSLSEQISFLEBQLGSCCKKDS 273
241 VHSFOQLGRIDSLSEQISFLEBQLGSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLEBQLGSCCKKDS 273

RESULT 14
AA411771
ID AA411771 standard; Protein; 273 AA.
XX
AC AA411771;
XX
DT 07-DEC-1999 (first entry)
XX
XX Human PRO1449 protein sequence.
DE Human PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
XX 16-SEP-1999.
PD
XX
PF 08-MAR-1999; 99WO-US05028.
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XX 10-MAR-1998; 98US-0077450.
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PR 11-MAR-1998; 98US-0077632.
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PR 11-MAR-1998; 98US-007641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
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PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
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PR 30-MAR-1998; 98US-0079923.
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PR 01-APR-1998; 98US-0080328.
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PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083559.
PR 05-MAY-1998; 98US-0083742.
PR 06-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.

PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
PA (GETH) GENENTECH INC.
XX
XX
FI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI, 1999-551358/46.
DR N-PSDB; AA234313.
XX
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX
PS Claim 12; Fig 217; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA233891 to
XX AA234318, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
SQ Sequence 273 AA;
Query Match 99.9%; Score 1504; DB 20; Length 273;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSGQEVLLMWLTLVAVGTEHAYRGRRCVCAVAHGDVSESVQRYQPFLLTCDGHR 60
DB 1 MRSGQEVLLMWLTLVAVGTEHAYRGRRCVCAVAHGDVSESVQRYQPFLLTCDGHR 60
QY 61 ACSYRRTYRPAVRSGLAPARPRVACCPGKRTSLPGACGAATQPPCRNGSCVOP 120
DB 61 ACSYRRTYRPAVRSGLAPARPRVACCPGKRTSLPGACGAATQPPCRNGSCVOP 120
QY 121 GRRCRPAWGRDTCQSDVDECSARAGGCPORCINTAGSYWCQEGHSLADGTLCPYKG 180
DB 121 GRRCRPAWGRDTCQSDVDECSARAGGCPORCINTAGSYWCQEGHSLADGTLCPYKG 180
QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVLLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVLLLEKQLVLAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDSLEQISFLEQIGSCCKKDS 273
DB 241 VHSFOQLGRIDSLEQISFLEQIGSCCKKDS 273
RESULT 15
ID AA08381 standard; Protein; 273 AA.
XX
XX AA08381;
AC
XX
DT 26-APR-1999 (first entry)

```

XX Human neuro-growth factor-like protein Zneul.
DE
XX
XX Zneul-1; neuro-growth factor-like protein; human; breast cancer;
KW glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
KW nerve regeneration; haematopoiesis; fertility; contraception;
KW antibody.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT /note= "putative signal peptide"
FT 20..273
FT Protein
FT /note= "mature protein"
FT 20..104
FT /note= "hydrophilic domain (HSM1), homologous to
FT an HSMC3W5A domain "
FT 105..135
FT /note= "epidermal growth factor-like domain 1"
FT 135..177
FT /note= "epidermal growth factor-like domain 2"
FT 178..273
FT /note= "domain HSM2 homologous to an HSMC3W5A
FT domain"
XX
XX MO9857983-A2.
XX
XX 23-DEC-1998.
XX
XX 18-JUN-1998; 98MO-US12763.
XX
XX 18-JUN-1997; 97US-0878322.
XX 18-JUN-1997; 97US-0050143.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Blumberg H, Jelinek LJ, Lehner JM, Shepard PO;
XX Whitmore TE;
XX
XX WPI; 1999-095324/08.
XX N-PSDB; AAV84341.
XX
XX New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's
XX disease, cancer and to repopulate blood cells
XX
XX Claim 6; Page 47-48; 70pp; English.
XX
XX This polypeptide comprises human Zneul, a new neuro-growth factor-
XX like protein. Its amino acid sequence was deduced from the
XX nucleotide sequence (see AAV84341) of a cDNA clone isolated from a
XX brain cDNA library. Zneul's closest human homologue is HSMC3W5A,
XX a gene in the HLA class III region, which is contained in a cosmid
XX which contains Notch 4. Zneul is also homologous to Notch 4 in its
XX EGF-like domains and may be involved in EGF receptor pathways.
XX Zneul is widely expressed in adult tissues, with high expression in
XX heart, placenta, spleen, testis, thyroid, spinal cord and lymph
XX node. Zneul polypeptide can be used as a growth, maintenance, or
XX differentiation factor in the spinal cord, heart, spleen, testis,
XX thyroid and lymph nodes. It may also play a role in breast cancer,
XX glioblastomas, and pituitary adenomas. Zneul may be used to treat
XX Alzheimer's disease, cancer, to repopulate blood cells after
XX chemotherapy, to stimulate myofibroblast proliferation, stimulate
XX or inhibit growth factors made in the placenta, in fertility and
XX contraception, or to regenerate nerves. Claimed Zneul
XX polypeptides (see also AAV8382-97), including specific domains of
XX Zneul and epitope-bearing portions of Zneul, can be used to raise
XX specific antibodies for use e.g. in diagnostic assays.
XX
XX Sequence 273 AA:

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Query Match 99.9%; Score 1504; DB 20; Length 273;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;

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Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGSQEVLMLLVAVGTEHAYRPGRRVCAVRAHGDVSESFVQRYVQPLTTCGHR 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MEGSQEVLMLLVAVGTEHAYRPGRRVCAVRAHGDVSESFVQRYVQPLTTCGHR 60
QY 61 ACSTYRTTYRTAYRRSPGLAPRPRVYACCPGKRTSSGLPGACGAAICQPPCRNGSCVQP 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ACSTYRTTYRTAYRRSPGLAPRPRVYACCPGKRTSSGLPGACGAAICQPPCRNGSCVQP 120
QY 121 GRCRCPPAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQMEGHSLSADGTLCPKG 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 GRCRCPPAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQMEGHSLSADGTLCPKG 180
QY 181 GPPRYVAPNPTGVDSAMKEEVORLQSRVDLLEBKQLVLIAPLHSLASQALEHGLPDGSL 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 GPPRYVAPNPTGVDSAMKEEVORLQSRVDLLEBKQLVLIAPLHSLASQALEHGLPDGSL 240
QY 241 VHSFQQLGRIDSLSEQISFLEEQUGSCGCKXDS 273
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 VHSFQQLGRIDSLSEQISFLEEQUGSCGCKXDS 273

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Search completed: September 10, 2003, 17:13:01
Job time : 67 secs